<b>STIC-Biotec</b>	h/ChemLib	1- (50	
From: Sent: To: Cc: Subject:	Fredman, Jeffrey Tuesday, September 17 STIC-Biotech/ChemLib Leffers, Gerald FW: 09/846,456	, 2002 2:36 PM	
PLEASE RUSH	<b>4</b> .		
I Approve.			
Jeff Fredman			CRIFE
Original Messa	_		
From: Sent: To: Subject:	Leffers, Gerald Tuesday, September 17, 2002 2:27 PM Fredman, Jeffrey RE: 09/846,456		
SEQ ID NO: 1	restricting because 1) the other seque (i.e. SEQ ID NO: 1 is a genomic gene d exon, etc.) and 2) the case has alrea quences (the case is at the stage of el	sequence; SEQ ID NO. 3 co adv been restricted by anothe	omprised within the whole ABC1 gene of orresponds to the first exon, SEQ ID NO: er examiner without restriction based is, Gerry
Gerald G. Leffers C Examiner, Art U Crystal Mall 1, 703-308-6232	Unit 1636		
Original	Message		
From:	Fredman, Jeffrey		
Sent:	Tuesday, September 17, 2002 2:24 PM		
To: Subject:	Leffers, Gerald RE: 09/846,456		
Gerald, Given sequence?		ing between the sequences	and requiring election of a single DNA
Jeff			
From: Sent: To:	iginal Message Leffers, Gerald Tuesday, September 17, 2002 2:05 PM Fredman, Jeffrey t: 09/846,456		
directe one of specifi some	ed to the whole sequence, or alternati f SEQ ID NOS: 1-5. SEQ ID NOS: 3-	vely, a polynucleotide compr 5 should be comprised within if SEQ ID NO: 2 is found wit uences in the case and dete	rmine if a single oligo search of SEQ 10
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	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher: D. Schriber	NA Sequences:	STN:
Phone: 308-4292	AA Sequences:	DIALOG:
Location: CM ( 6A0 3	Structures:	Questel/Orbit:
Date Picked Up: 9 18	Bibliographic:	DRLink:
Date Completed: 9120	Litigation:	Lexis/Nexis:
Searcher Prep/Review: 14	Full text:	Sequence Sys.: Compage
Clerical:	Patent Family:	www/internet:
Online time: 4	Other:	Other (specify):

24 30

Perfect score: Sequence: Scoring table:

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Run on:

Total number

Database

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Searched:

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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NoV-2001;
Aventis Pharma S.A. (FR)
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of Diministry 100.00, from No.0, 331; Conservative 0; Mismatches 0; Indels 0; Ga	acagggcatggtggcaggtgcctgtaatctcagttactcgggaggtggaggttgcaatga 	gcccagatcgcaccattgcactccagcctgggcaacaaaaggtgaaactccatctcaatt 	aaaaaaaaagaatgattttggtggtcgacttcaaataggtagg	agatggagggtcagggatctaattactctctaaaatcatgctaggaaagataacacct 	tttaataacactctctgcttttataacatcattctgccaaggagctcaaaggtttcaaca 	aagttcactttcagaaaaccctttgaggaagacagaatatacatcttctccatttta 	aagatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcactttgggagg 	ctgaggccagaggatcgcttgagctccagagtttgagaccagcctggataacatggcaaa 	acctftctctacaaaaaaatacaaaattagatgggtgtggtggcatgcacctgtggt 	cccagctacttgggaggctaaggtgggaggatcgcttgagcccagggagtcaagtctaca 	ctgagccatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctca 	aaaaaaagaaatgaaagaaagaaagaaagaaagagagag	gagggggggggaaggaaggaaggaaggaaggaaaaaaaa	gatgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaagtttga 	ccccaaaacccaatttattgaccaaggttattctttgactgaggcaaggggtccgctct 	cctgggccttgggctttagaaagctcatctctggcctttctgagatccatcc	ttattttttttgacacggagtcttgctctgtcactcaggctggagtgcagggggatgatc
tches	п п	61	121	181	241	301	361	421	481	541	601	661	721	781	841	901	196
Ma	Oy Db	oy Op	Qy Dp	oy D	Qy Db	O.y D.b	O.Y	Qy Dp	Oy Dp	O.y	Oy Db	oy Ob	Oy Dp	oy G	Qy Dp	Q.y Db	δy

Qy	1021	cgactcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcctcctga 108
QQ	1021	TCGACTCACTGTAACTCTGCCTCCCGGGTTCAGCGATTCTCCTGCCTCAGCCTCCTGA 1080
ΟŶ	1081	taacaggcgccgccacactctggctaattt
QO	1081	ATAACAGGGGCCCCCCACCACCATCTGGGCTAATTTTTGTTTTTTAGTAAGACTGGGTT 11
Qy	1141	ō
Db	1141	CATCATGITGGCCAGGTTGGTTTCGAACTCCTGACGTGAGGTGAG
δy	1201	ctcccaaagtgctgggattacaggcatgagccactgcgcccagctcagatccattt 1260
QQ	1201	TCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCCAGGTCCATCCA
δλ	1261	
QQ	1261	TAAGGGCAAACAGTCCATGGTGCAAAGGGGCCCATGCCACCCAGAGTTATGAGTACCTGG 132
QY	1321	tccagaattccttgcctggtggcctccacatgcacttccagggcctgcttgggcctc 13
QQ	1321	ACTCCAGAATTCCTTGCCTGGTGGCCTCCATGCACTTCCAGGGCCTGCTTGGGCCTC 138
QY	1381	tatgcgtctgtcctgagtgttgatagaaccactgatgtgagtacctgggcttgagcc 144
qq	1381	ICTATGCGTCTGTCCTGAGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGCC 144
ογ	1441	tggcctggagatcctgttgactgtagcatggagggggcttgttgtgcagctgaatgtctgca 150
qq	1441	GGAGAICCTGTTGACTGTAGCATGGAGGGGGCTTGTGCAGCTGAATGTCTGCA 150
δ	1501	caggtggtgggagttctggaatatgatggagctggaagtgggaagaagtaggcttg 15
qq	1501	GLAGGTGGGGAGTTCTGGAATATGATGGAGCTGGAGGTGGGAAAGAGGAAGTTGCTTG 156
Qy	1561	ggcagctctctcatgccacctcattctggccaaaactcaggtcaaactgtgaagagtct 162
QQ	1561	GCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCT 16
QY	1621	tttgtcaaggtaggagacctt 1
QQ	1621	IGTGAATCTGCCTTCAAGGTGGCTACAAGGTATCTTTGTCAAGGTAGGAACCTT
οy	1681	ttccagggcctg
qq	1681	TGGCCTCCACGTGCACTTCCAGGGCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGT 174
Οy	1741	tatgaatccttcagggcagattcatatttagactcttcacagtttgacctgagttt 18
qq	1741	ITCTATGAATCCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTT 18
	1801	ccagaataaggtgacatttagtttgttggcttgatggatg
qq	1801	GGCCAGAATAAGGTGACATTTAGTTTGTTGGCTTGATGGATG
QY	1861	ggtgtgtaggcctgcattcctactcttgccttttttttgcccctccagtgttttg
qq	1861	GTGTAGGCCTGCATTCCTACTCTTGCCTTTTTTTTTTTGCCCCTCCAGTGTTTTGGGT 19
QY	1921	ttttgctccctacagccaaaggcaaacagagaagttggag
ΩD	1921	ITTGCTCCCCTACAGCCAAAGGCAAACAGAGAAGTTGGAGGTCTGGAGTGGCTACAT 1
Qy	1981	aattttacacgactgcaattctctggctgcacttcacaaatgtatacaaaactaaatacaa 2040
QQ	1981	ITTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATAAA
Qy	2041	gtcctgtgtttttatcacagggaggctgatcaatataatgaaattaaaggagctggtc 2100
QO	2041	CTGTGTTTTTTATCACAGGGGGGCTGATCAATATAATGAAATTAAAAGGGGGCCTGGT

Qy Db

οy

0.y 0.y 0.b

Qy Db

RESULT 2 AX092589 LOCUS AX092589 AX092589 AX092589 AX092589 AX092589 AX092589 LOCUS AX092589 AX09268 AX092589 AX09268 AX0926	Ouery Match  Best Local Similarity 98.0%; Pred, No. 0.  Matches 3183; Conservative 10; Mismatches 37; Indels 18; Gaps 3;  Matches 3183; Conservative 10; Mismatches 37; Indels 18; Gaps 51;  Oy 2 cagggcatggtgcagtgcctgtaatctcagttactcgggaggtggaggtggaggttgcaatgag 61  Inililililililililililililililililililil	Db 26360 cccrdrcracadadadadacadadrracardagardegrargeracargeracrgragger 26419  Qy 542 ccaqctacttgggaggtctaaggtggaggatcgcttgagcccagggagtcaagtctacac 601
2101 catattgttctgttttttttttttttttttttttttttt	ggctgccgggaacgtggactagaggtctgcggcagcccggagccaggccttcccgc gcgtcttaggccgggaccagaggtctgcggcgaccccgagcccagaccttcccgc gcgtcttaggccggggcccggggggaggaaggaagccggaccctaagaca	Addictroftcandidationsatandance.cantcandant.communicationsatandandandandandandandandandandandandanda

Qy Db QΥ QΩ

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61 6539 10 6599 70 6659	30 6719 90	6779 50 6839	010 6899	070 5959	130 7019	90.	139	110	70 259	30 319	90 379	50 439	10 499	70 559	30
tgagccatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctcaa 6	aaaaacaagatgaaacagagcagaaagactttacgtaaattgctcatcatgtggttg 8	CAGGTTTGACCCCAAAACCCAATTTTTTTTGACCAGGTTATTTTGACTGAGGCAAGGG 2  1 CCGCCCCCCCGGGGGCCCTTAGGGGGGCCCCCCCCGGGCCCTTGACTGAC	ttatttttttttgacacggagtcttgctctgtcactcaggctggagtgcag 1 	ggcatgatetegacteactgtaacetetgeeteegggtteaagegatteteetgeete 10 	goctoctgagataacaggogocogocaccacatotgoctaatttttgtatttttagtaa 11 	<pre>gactgggtttcatcatgttggccaggttggtttcgaactcctgacctgaggtgagctgc 11                                    </pre>	cacettggcctcccaaatgctgggattacaggcatgagccactgcgcccagctcagat 12 	catccctttctaagggcaaacagtccatggtgcaaaggggccatgccacccagagttat 13 	agtacctgggactccagaattccttgcctggtggcctcacatgcacttccagggcctg 13 	ttgggcctcttctatgcgtctgtcctggtgttgatagaaccactgatgtagtactg 14 	<pre>icttgagccgtggcctggagatcctgttgactgtagcatggaggggcttgtgcagctg 14                                     </pre>	atgtctgcatgcaggtggtgggagttctggaatatgatggagctggaggtgggaaga 15 	gtaggcttggggcagctctctcatgccacctcattctggccaaaactcaggtcaaactg 16 	aagagtctaaatgtgaatctgccttcaaggtggctacaaaggtatctttgtcaaggt 16 	gagaccttgtggcctccacgtgcacttccagggcctgcttgggcctcttct
602 t 26480 T 662 a 662 a 711 g 711 g	1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	26720 ric 891 go 1 26780 GC	951 C	1011 to	1071 ag   26960 AG	1131 aç   27020 AC	1191 cc 	1251 cc     27140 CC	1311 ga 	1371 ct 	1431 gg    27320 GG	1491 aa     27380 AA	1551 ag    27440 AG	1611 tg    27500 TG	1671 ag '
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Oy Oy	90 A	Oy Dp	Oy Dp	Oy Dp	Qy Dp	Qy Dp	Qy Dp	Qy	Qy	Oy Db	Oy Dp	Qy Db	Oy Dp	οy

27620 IGTCCIGAGICITCIAIGNAAICIGICCITCAGGGCAGAITCAIAITIAGACICIICACA 27679 27919 28279 ---tccttcagggcagattcatatttagactcttcaca 1785 CGGCTGAGGAAACTAACAAAGGAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAA 28399 2263 28580 CCAACTCCCTAGAIGIGGICGIGGGCGCTGAACGICGCCCGTTTAAGGGGCCGGCCCCGG 28639 ttaaatatttagac--atggtgtgtgtaggcctgcattcctactcttgcctttttttgcc 1903 1963 gtctggagtggctacataattttacacgactgcaattctctggctgcacttcacaaatgt 2023 2383 2443 2803 cctccagtgtttttgggtagttttgctccctacagccaaaggcaaacagagaagttggag 2204 tegggteetetgagggacetggggageteaggetgggaatetecaaggeagtaggtegee 18100 TCCGGTCCTCTGAGGACCTGGGAACCTCAGGCAGCTGGGAATCTCCAAGGCAGTAGGTCGCC 2564 agcccagcgcttcccgcgcgtcttaggccggcgggccgggggggaagggaacgcaga tttttgtttttgtggcctccttcctctaaatttatgaagaagcagtaagatgttcctc cggctgaggaaactaacaaaggaaaaaaattgcggaaagcaggatttagaggaagcaa tgtcctgagtcttctatgaa-1731 1846 2144 1964 1904 2444 2624 28340 2504 28400 2684 qq δλ δ g ò g οy Ω δ q Qγ g ŏ qq δ qq δ a δ QQ g Dp δy δy g Q δ οy δ g g g δ ŏ δy

셤

δŏ a 임

δ

qq

QY

g δλ g δ q δŏ

δ

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http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
sections only once, except for a short overlap.
The true right end of clone RPI1-21787 is at 96717 in this
sequence. The true left end of clone RPI1-21787 is at 96717 in this
sequence. The true left end of clone RPI1-127810 is at 72980 in
this sequence. The true right end of clone RPI1-31320 is at 2000 in
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                            http://www.sanger.ac.uk/HGP/Chr9
RP11-217B7 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derived from a single pUC clone. Restriction digest data confirm\ the\ assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19791 AGATGAAGAAACAGGCCGGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGGAGGC 19732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20151 CCGGGCATGGTGGCAGGTGCCTGTAATCTCAGCTACTCGGGAGGTGGAGGTTGCAATGAG 20092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA." 84273
Anote-"Sequence from overlapping clone RP11-122F10
(AC026643). Assembly confirmed by restriction digest." 92050. 92163
/note-"Sequence from reads from a short insert library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 agatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcactttgggaggc 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ttaataacactctctgcttttataacatcattctgccaaggagctcaaaggtttcaacaa 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 cccagatcgcaccattgcactccagcctgggcaacaaaaggtgaaactccatctcaatta 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 tgaggccagaggatcgcttgagctccagagtttgagaccagcctggataacatggcaaaa 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Sequence from AF275948 sequenced by National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 cagggcatggtggcaggtgcctgtaatctcagttactcgggaggtggaggttgcaatgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 gatggagggtcagggagatctaattactctctaaaatcatgctaggaaagataacacctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 96717;
                                Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.6%; Score 3121.6; Best Local Similarity 98.8%; Pred. No. 0; Matches 3207; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     confirm the assembly."
27673 a 21138 c 20380 g 27526
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. 96717
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-217B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .92557
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ORIGIN
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humquery@sanger.ac.uk Clone requests. clonerequest@sanger.ac.uk
n Jan 15, 2002 this sequence version replaced $\frac{9}{1}\displays1812468\dots
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORWPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRI 11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL359182 96717 bp DNA linear PRI 11-JAN-2007
Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                           28880 CCGCGCACCAACAGAGCCGGTTCTCAGGCGCCTTTGCTCCTTGTTTTTTCCCCGGTTCTG 28939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28940 TTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAAAGAGACGCAMACACAAAA 28999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29060 GCCAAGGAGGCTTCGGGAAGTGCTCGGTTTCGGGGACTTTGATCCGGAGCCCCACATCCC 29119
     28640 CTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGGGGCGGG 28699
                                                                                                                                                                                                                                                                                          ccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttccccggttctg 3043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttttctccccttctccggaaggcttgtcaaggggtaggagaaagagacgcaaacacaaaa 3103
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                                                                                                                                                                                                                                                                                                                       gtggaaaaacaggtaaagaggctctccagtgacttacttgggcgttattgttttgtttcgag
                                                                                                                                                                            AL359182.20 GI:18151453
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LOCUS
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ORGANISM
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6 tttgtttt 	tttgttt         TTTGTTT
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mRNA

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exon

CDS

Location/Qualifiers 1. .201144 /organism="Homo sapiens"

FEATURES Source

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HHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLSSCRNSS
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                                                                                                                                                                                                                                                                                            Score 2955.2; DB 9; Length 201144;
                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                0; Mismatches 121; Indels
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Best Local 9
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602	662	722 31787	782	842 31907	902 31967	962 32027	1022 32087	1082 32147	1142 32207	1202 32267	1262 32327	1322 32387	1382	1442 32507	1502 32567	1562 32627	1622 32687
Qy	Oy Ob	Oy Ob	Oy Op	oy Ob	ΟΥ Db	Qy Db	Qy Db	Oy Dp	Qy Db	Qy Dp	Qy Db	Qy	Qy Db	Qy Db	Qy Dp	Oy Dp	Qy Db

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Dy 2818 caggacttcgaccgatagtaacctcggactcggtcgaccgaactcataaaaggaactag 2877  Dy 2878 [	tch al Similarity 100.0%; Fred. No. 0; 2893; Conservative 0; Mismatches acaggacatggtagaggtgctgtaattcagttac

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Creng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschlid,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
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Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
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Best Local Similarity 98.1%; Pred. No. 0;
Matches 1615; Conservative 0; Mismatches
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                    AX060715 1643 bp
Sequence 3 from Patent W00078972.
AX060715
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Location/Qualifiers
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PAT 22-JAN-2001

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RESULT AX060894 LOCUS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Arb binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1525 atgatggagctggaggtgggaagagaagtaggcttggggcagctctctcatgccacctca 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggctacaaaggtatctttgtcaaggtaggagaccttgtgggcctccacgtgcacttccagg 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccaaaggcaaacagagaagttggaggtctggagtggctacataattttacacgactgcaa 1998
                                                                                                                                                                                                                                                                                                 1405 gatagaaccactgatgtgagtacctgggcttgagccgtggcctggagatcctgttgactg 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 GGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGGCCTCCACGTGCACTTCCAGG 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 TAGCATGGAGGGGGCTTGT-CAGCTGAATGTCTGTATGCAGGTGGTGGGGGGTTCTGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 ATGATGGAGCTGGAAGGAAGAAGAAGTAGGCTTGGGGCAGCTCTCTCATGCCACCTCA
                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                     6; Length 1643;
                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                  Query Match
46.0%; Score 1485.4;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1615; Conservative 0; Mismatches
                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
Sequence 3 from Patent WO0078971.
AX060894
                                                                                                                                                                                                     457 g
                          AX060894.1 GI:12406271
                                                                                                                                                                                                       413 c
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                                                                                                                                                                                                      BASE COUNT
ORIGIN
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HTG 22-APR-2000
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
pieces.
                                                                                                                                                                                           2237
                                                                                                                                                                                                                                                   gocogggoggggaaggggacgcagaccgcgggaccctaagacacctgctgtaccctccac 2657
                                                                                                                                                                                                                                                                                                                                                                                     tegecegtttaagggeegggeceggetecacgtgetttetgetgagtgaetgaactaca 2777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cctctgcgctcggtgcagccgaatctataaaaggaactagtcccggcaaaaaccccgtaa 2897
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agggaggctgatcaatataatgaaattaaagggggctggt-ccatattgttctgtgttt
                  731 AGGGAGCTGATCAATATAATGAAATTAAAAGGGGCCTGGTCCCATATTGTTCTGTGTTT
                                                                                    2298 aacaaaagcagcccattacccagaggactgtccgccttcccctcaccccagcctaggcct
                                                                                                                                                               gctctctctcccccaatccctccctccggctgaggaaactaacaaaggaaaaaattg
                                                                                                                                                                                                                                                                                                                                                           2118 tigittigttigttigttigttictttittigttittigtgicctccticctccaattia
                                                        tgaagaagaagcagtaagatgttcctctcgggtcctctgagggacctggggagctcaggct
                                                                                                                gggaatctccaaggcagtaggtcgcctatcaaaaatcaaagtccaggtttgtggggggaa
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AC012230.3 GI:7637254
HTG; HTGS_PHASE1; HTGS_DRAFT.
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SOURCE

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97902 98001; gap of 100 bp 100
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157492 175064; contig of 17573 bp in length.
Location/Qualifiers
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f 5125 bp in length
8: gap of 100 bp
7200: contig of 1872 bp in length
                                                                                                                                                                                                                                                     100 bp
3054 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                       o of 100 bp
contig of 4417 bp in length
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contig of 2943 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 100 bp contig of 4676 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37; gap of 100 bp 71458; contig of 2921 bp in length 58; gap of 100 bp 76888; contig of 5330 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p of 100 bp contig of 6007 bp in length
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93499: contig of 5179 bp in length
                                                                                                                                                                                                                                                                                                                                     in length
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38318: contig of 3919 bp in length
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/clone_lib="RPCI-11 Human Male
                                                                                                                                                                                                        100 bp
2377 bp
                                               p of 100 bp
contig of 2831 bp
                                                                                                    p of 100 bp
contig of 2356 bp
                                                                                                                                                                                                                                                                                                          p of 100 bp
contig of 2861 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            p of 100 bp
contig of 2513 bp
                                                                                                                                                    87: gap of 100 bp 25707: contig of 3020 bp
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45549 48116: contig of 2568 bp
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2735. .4415
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                contig of
                                                                                                                                                                                                                                                                                  contig of
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                                     42835: cor
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                                                                                                                                                                                                                                                284: gap of
31338: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56593 56692: gap of 56693 59635: cont
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82113: conf
                                                                                                    20231: gap of
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34299: con1
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18217 52618: con
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38419 4283
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                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Coastle, A., Colangelo, M., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Mordonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., Mcdanglin, J., Maldin, J., Mallor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 185000; agarose fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; agarose fp
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project incommentation
Center clone name: 1.2510
Center clone name: 1.24.10
Center clone name: 1.24.10
Center clone name: 1.24.10
Sequencing vector: 1.31; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 117571 bases at least Q40
Consensus quality: 145749 bases at least Q30
Consensus quality: 160940 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Web site: http://www-seq.wi.mit.edu
Web site: sequence.submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1003: contig of 1003 bp in length
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of 1531 bp in length
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                                                                                                                      Birren, B., Linton, L., Nusbaum, C. and Lander, B. Homo sapiens, clone RP11-1M10
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
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4516 5785: con
5786 5885: gap of
5886 7879: con
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15228: con
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COMMENT

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HSA252201 1167 bp DNA linear PRI Homo sapiens partial ABC-1 gene for ATP-binding cassette
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Pred. No. 8.2e-311;
0; Mismatches 2;
                        5886. .7879

/note-"assembly_fragment"

/980. .9686

/note-"assembly_fragment"

9787. .12253

/note-"assembly_fragment"

/1354. .15228

/note-"assembly_fragment"

15329-".17200
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25808. .28184
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28285. .31338
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31439. .34299
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34400. .38318
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4516. .5785
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5886. .7879
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20232. .22587
/note="assembly_fragment"
22688. .25707
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17301. .20131
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38419. .42835
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42936. .45448
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18217. .52618
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/note="assembly_fragment"
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/note="assembly_fragment
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71559. .76888
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Best Local Similarity 98.7%;
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                                                            GCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTACATAAACAGAGGCCGGG
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353 ACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCCTTTGAAAGGAAACAAAG 412

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1 (bases 1 to 1167)
Porsch-Ozcurumez,M., Langmann,T., Heimerl,S., Borsukova,H.,
Porsch-Ozcurumez,M., Langmann,T., Heimerl,S., Borsukova,H.,
Kaminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G.
The zinc finger protein 202 (znf202) is a transcriptional repressor
of atp binding cassette transporter al (abcal) and abcgl gene
expression and a modulator of cellular lipid efflux
J. Biol. Chem. 276 (15), 12427-12433 (2001)
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                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for
Clinical Chemistry, Universitiy of Regensburg,
FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1955 aagttggaggtctggagtggctacataattttacacgactgcaattctctggctgcactt 2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="cholesterol efflux regulatory protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="cholesterol efflux regulatory protein"
315 c 327 q 247 t
                 AJ252201. GI:12053757
AJS52201.1 GI:12053757
ABC-1 gene; ATP-binding cassette transporter-1; promoter.
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 promoter region
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="leukocyte"
1. .1167
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/chromosome="9"
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transporter-1, 5'UTR and
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Porsch-Oezcueruemez, M.K.
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1148. .1167
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/qene="ABC-1"
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AF258623S1 1167 bp DNA linear PRI 23-JUN-2000 monographic assette transporter 1 (ABCAL) gene,
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Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Audizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of habCl gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
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708 CACCTCCCCCAACTCCCTAGATGTGTGTGGGGGGGGGTGAACGTCGCCCGTTTAAGGGGC 767
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                                                                                                                                                                                                                                                                              aggaagcaaattccactggtgcccttggctgccgggaacgtggaactagaagtctgcggc
                                                                                                      cacctcccccaactccctagatgtgtcgtgggcggctgaacgtcgcccgtttaaggggc
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AF258623.2 GI:8677405
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                                                                          Submitted (20-APR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
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                                                                                                                   Tunical (bases I to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Direct Submission
Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue,
Francisco, CA 94143-0130, USA
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                                                                                                                                                                                                                                    Sequence update by submitter
On Jun 23, 2000 this sequence version replaced gi:7769713.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Length 1167;
Biochem. Biophys. Res. Commun. 271 (2000) In press 2. (bases 224 to 1167)
Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng.C., Aquizerat,B.E., Fielding,C.J. and Kane,J.P.
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Pred. No. 9.3e-286;
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barner, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Downion, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehockky, J., Levine, R., McGurk, A., McKernan, K., McChara, R., Meduis, N., McEwan, P., McGurk, A., McKernan, K., McChara, C., Liou, G., Liou, G., Locke, K., Madonald, P., Maddis, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, T., O'Lowie, R., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
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1 (bases 1 to 69570)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome, clone RP11-1N10

Unpublished
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                                     ACO21246 69570 bp DNA linear HTG 1
Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
ACO21246
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HTG; HTGS_PHASE0.
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COMMENT

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Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                  ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                  Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705871. All repeats were identified sing RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2512
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66: gap of 100 bp
20921: contig of 855 bp
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                                            Tirrell, A., Vassiliev
Zimmer, A. and Zody, M.
Direct Submission
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AC012230 175064 bp DNA linear HTG 22-APR-2000 Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175064)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-1M10
                                                                                                       41705 CCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGAGCC 41764
                                  Center clone name: 1_M_10

Center clone name: 1_M_10

Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 11571 bases at least Q40
Consensus quality: 145749 bases at least Q20
Consensus quality: 160940 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBK
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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100 bp 6672 bp in length

22

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117.08 124.79; contig of 6672 bp in length 124.08 124.79; contig of 100 bp 124.180 131281 contig of 7102 bp in length 131.282 131381; gap of 100 bp 131882 131859; contig of 6678 bp in length 131860 138159; gap of 100 bp 138160 145491; contig of 7332 bp in length 145492 145591; gap of 100 bp 16732 157391; contig of 138100 bp in length 157392 1573491; gap of 100 bp 157392 157491; gap of 160 bp 167573 bp in length
                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11 Human Male BAC"
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22688. .25707
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1104. .2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5886. .7879
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7980. .9686
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15329. .17200
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17301. .20131
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/note="assembly_fragment"
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52719. .56592
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                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-1M10"
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71559. .76888
                    117308 117407: gap of 117408 124079: cont
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NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                             2635 2734: gap of 100 bp 2735 4415: contig of 1681 bp in length 4416 4515 5785: contig of 1270 bp in length 5786 5885: gap of 1270 bp in length 5880 7979: contig of 1994 bp in length 7880 7979: contig of 1994 bp in length 7980 9686: contig of 1707 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25707: contig of 3020 bp in length 807: gap of 100 bp 28184: contig of 3020 bp in length
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                                                                                                                                                                              of 100 bp
contig of 1531 bp in length
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22587: contig of 2356 bp in length
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2377 bp in length
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31338: contig of 3054 bp in length
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2936 45448: contig of 2513 bp in length
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56592: contig of 3874 bp in length
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68437: contig of 4676 bp in length
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5330 bp in length
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4302 bp in length
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4417 bp in length
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contig of 2943 bp in length
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contig of 2921 bp in length
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98002 103016: contig of 5015 bp in length
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12253: contig of
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93499: ~
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17301 20131: cont
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97901: con
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59636
59736
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Length 175064;

DB 2;

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HTG 13-JUL-2000
                1;
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                              1618 CCCAGATCGCACCATTGCACTCCAGCCTGGGCAACAAAAGGTGAAACTCCATCTCAATTA 1559
                                                                                                                                                                                                                                                                                               1438 TTAATAACACTCTCTGCTTTTATAACATCATTCTGCCAAGGAGCTCAAAGGTTTCAACAA 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                            481
                                                                                                                                                                                                                                                                   ttaataacactctctgcttttataacatcattctgccaaggagctcaaaggtttcaacaa 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccctgtctctacaaaaaaaaatacaaaaattagatgggtgtggtggcatgcacctgtggtc 541
                                                                                                cccagatcgcaccattgcactccagcctgggcaacaaaaggtgaaactccatctcaatta 121
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            tgaggccagaggatcgcttgagctccagagtttgagaccagcctggataacatggcaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602 tgagccatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctcaa
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Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
                1;
                Indels
 Pred. No. 5.7e-134;
0; Mismatches 107;
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              Matches 569; Conservative
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Best Local Similarity
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TITLE
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REFERENCE
AUTHORS
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Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Flerre, N., Subramanlan, A., Talamas, J., Teefaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ve, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced 91:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2512
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                                                                                                                                                                                                                  HTG 13-JUL-2000
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                    90698 bp DNA linear HTG 1
HOMO Sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
AC021345.2 GI:9130845
HTG; HTGS DIRECT DIRECT
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-24J9
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COMMENT

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3 3347: contig or by 3 3447: contig or by 33447: contig of bp 18 334435: contig of 888 bp in length 36 3535: gap of 100 bp 354335: contig of 898 bp in length 36 35433: contig of 898 bp in length 36 35433: contig of 907 bp in length
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37422: contig of 882 bp
37522: gap of 100 bp
38402: contig of 880 bp
38502: gap of 100 bp
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31453: contig of 906 bp
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10 51309; contig of 899 bp in length 10 51309; gap of 100 bp 10 5221; contig of 912 bp in length 10 5231; gap of 100 bp 10 53305; contig of 884 bp in length 10 53305; contig of 884 bp in length 100 bp 100 
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                                                                                                                                                                                                                                        100 bp
f 894 bp in length
100 bp
f 858 bp in length
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65975: contig of 860 bp in length
66075: gap of 100 bp
66954: contig of 879 bp in length
67054: gap of 100 bp
67947: contig of 893 bp in length
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                                         39381 39480: gap of 100 bp
4441 44040: contig of 927 bp in length
40408 40507: gap of 100 bp
40508 41405: contig of 898 bp in length
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39380: contig of 878 bp in length
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contig of 887 bp
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Query Match
Best Local Similarity 90.8%; Pred. No. 2.3e-114;
Matches 543; Conservative 0; Mismatches 49; Indels 6; Gaps

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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LXR. (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates or RXR-mediated transcriptional activity -

Claim 8; Fig 1; 317pp; English.

selected a The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selection normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.

Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;

э; 25999 26479 421 301 481 541 770 cccagatcgcaccattgcactccagcctgggcaacaaaaggtgaaactccatctcaatta 121 61 DB 22; Length 183999, cagggcatggtggcaggtgcctgtaatctcagttactcggggaggtggaggttgcaatgag cccagatogcaccattgcactccagcctgggcaacaaaaggtgaaactccatctcaatta gatggagggtcagggagatctaattactctcaaaatcatgctaggaaagataacacctt gatggagggtcasggagatctaattactctctaaaaatcatgctaggaaagataacacctt ttaataacactctctgcttttataacatcattctgccaaggagctcaaaggtttcaacaa agttcactttcagaaaacccctttgaggaagacagaatatacatcttctccattttaa tgaggccasargatcgcttgagctccaragtttgagaccagcctggataacatggcaaaa ccctgtctctacaaaaaaaaatacgaaaattagatgggtggtggcatgcacctgtggtc ccagctacttgggaggctaaggtgggaggatcgcttgagcccagggagtcaagtctacac tgagccatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctcaa tgaggccagaggatcgcttgagctccagagtttgagaccagcctggataacatggcaaaa 37; Indels 96.8%; Score 3127.8; 98.0%; Pred. No. 0; 10; Mismatches Best Local Similarity 98.08 Matches 3183; Conservative Query Match ~ 242 302 482 542 662 711 62 26000 26060 422 26360 26540 25940 182 26120 26180 362 26240 26300 26420 602 26480 g g q g ò 셤 g g qq δ õ ò ŏ ò ð g 8 g ò ò ò a ò ò ò

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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler Alsease, a genetic disorder characterised by abnormal HBL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays of screen for compounds that requlate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for a disorders associated with cholesterol transport. The genes and proteins are also useful for a disorder and disorders associated with cholesterol transport. The genes and cardiovascular disease and
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                                                                                16-JUN-2000;
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10; 1345 gectecacatgeacttecagggeetgettgggeetettetatgegtetgteetgagtgtt 1404 gatagaaccactgatgtgagtacctgggcttgagccgtggcctggagatcctgttgactg 1464 atgatggagctggaggtgggaagagagtaggcttggggcagctctctcatgcacctca 1584 ttctggccaaaactcaggtcaaactgtgaagagtctaaatgtgaatctgcccttcaaggt 1644 Gaps 192 atgatggagctggaggtgggaagaagtaggcttggggcagctctcatgccacctca 251 gatagaaccactgatgtgagtacctgggcttgag-cgtggcctggagatcctgttgactg Query Match 46.0%; Score 1485.4; DB 22; Length 1643; Best Local Similarity 98.1%; Pred. No. 5e-305; Matches 1615; Conservative 0; Mismatches 6; Indels 26; Query Match Best Local S 133 74 1465 1525 1585 1405 δ g òγ g δ q φ d Qγ

Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;

ggctacaaaggtatctttgtcaaggtaggagaccttgtggcctccacgtgcacttccagg 1704

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptrises: (a) an oligo-dT primer and an oligonuclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence complementary to a complementary strand of a period sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises a 1 least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and the primers allow obtaining of the full-length cDNAs absorbations and AAH13613 to AAH18712 represent human cDNA sequences; AAB92446 to
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                                    1497 cctctgcgctcggtgcagccgaatctataaaaggaactagtcccggcaaaaaccccgtaa 1556
                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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       cctctgcgctcggtgcagccgaatctataaaaggaactagtcccggcaaaaaccccgtaa
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Wakamatsu A, Nagai K,
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Sugiyama T, Wakamatsu
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2000JP-0118776.
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09-JUN-2000; 2000JP-0241899
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Ishii S,
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                                                             Length 763;
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, Otsuki T
                                              Sequence 763 BP; 137 A; 205 C; 260 G; 158 T; 3 other;
                                                                               10.4%; Score 336; DB 22; 100.0%; Pred. No. 9.1e-62;
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Wakamatsu
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27-AuG-1999; 99JP-0300253.
11-AAN-2000; 2000JP-0118776.
09-JUN-2000; 2000JP-0241899.
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                        of the present invention.
                                                                                                        Conservative
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The present invention describes primer sets for synthesising 5602 (ill-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence of an oligonucleotide which comprises a 1'-end sequence of sequence (sequence) and an oligonucleotide comprises a 1'-end sequence of the comprises a 1'-end sequence of polynucleotide which comprises a 1'-end sequence of the primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the price and old etection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and primers allow obtaining of the
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                                                                                                                 The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding including cancer.
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                                        olated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition
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                                                                                      Disclosure; SEQ ID NO 8043; 1297pp + Sequence Listing; English
                                                                                                                                                                                                                  Sequence 20645 BP; 5578 A; 4294 C; 4693 G; 6080 T; 0 other;
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       Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                        1141 tcatcatgttggccaggttggtttcgaactcctgacctgaggtgagctgccaccttggc 1200
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB1678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are nedical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune, hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collits; (c) cardiovascular disorders such as mycocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitate infections.

Orde: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
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cancers and metastases -
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375 ggccgggcacaatggctaatgcctgtaatcccagcactttgggaggctgaggccagagga 434

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1084 aacaggcgcccgccaccacatctggctaatttttgtatttttagtaaagactgggtttca 1143
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antidungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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2000US-0180628.
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2000US-0186350.
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the genes are The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune throughly cancer and other cancer of disease, allergies, cutoimmune disorders, neutoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatch arthritis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias;
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1larity 64.7%; Pred. No. 2.2e-59;
Conservative 0; Mismatches 302;
              08-DEC-2000; 2000US-0251868.

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                                                         2745 GCTGGGTAGAATCAGGGGCACTTGCTTTCCCGTGGAGGGTCTTCAGGTGACGTTCTTATC 2686
                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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792 ggcagaaagactttacgtaaattgctcatcatgtggttgtcaagtttgaccccaaaaaccc
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Rosen CA, Barash SC, Ruben SM

(HUMA-) HUMAN GENOME SCI INC

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 37020; 3071pp + Sequence Listing; English.

AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the

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represent sequences used in the exemplification of the present invention.
                         diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
   protein. (I) proteins and polynucleotides may be used to prevent,
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ABA19145 standard; DNA; 23934

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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialiaepetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiambetic; antime disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (ABA11004-ABA21534) and proteins
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuncer; vulnerary; anticonvulsant; antibacterial; antimogal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
20865 CATAAAATITICTACTITGGGAGACAGAAAAAATCATGGAAATGTTCCTTGAAAATTTT 20806
                                                                                                                                                                                                                                              20570 GCCTGGCTAATTTTTGTATTTTAGTAGACAGGGTTTTACCATGTTGGCCAGGCTGAT 20511
                                                                          20985 GTAGAAGTGATCAGATATTTATCTGCATAAATAATAAAGGTAGAAAGTAATTCATATT 20926
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                             20925 TAAGAAGGAACAATTGGGGTTTCATAACTCATGAAGAGTTAAATGAGTTCAAAAGAGGGA
                                                                                                                                                      871 ttctttgactgaggcaagggggtccgctctcctgggccttgggctttagaaagctcatct
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                                                                                          768 aagaaaaaaaaaaagatg-----aaacagaggcagaaagactttacgtaaattgctcat
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                                              Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including
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9 The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, of astrointestinal tract, liver, lung, or urogenital; (b) immune discretive contents autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple scalerosis, rheumatoid arthritis and ulcerative colitis; (a) wound help and allorders e.g. cerebral scheemias; (d) wound help colitish the colitish contents and epilepsy; (e) neurological diseases e.g. crebral anoxia and epilepsy; 2831 ggcggaggttgcagtgagccgagatcatgccactgcactctagcctggg-cgacagagca 2889 2594 tttctcacataaagaccttacttaggaggccagacgtggtggctcatgcctataatccca 2653 2654 gcactttgggaggccgaggctggcagatcgcttgagtgcaggagtttgagaccagcatgg 2713 2714 gcaacatggcgaaaccccatctctacaaaaata---caaaattaaccaggtgttgtggc 2770 2950 gtagaagtgatcagatatttatctgcataaataataaaaggtagaaagtaattcatatt 3009 cataaaattttctactttgggagacagaaaaatcatggaaatgttccttgaaaaatttt 3129 3130 attcagagatgaagccagaaggaactctgggttgaggagaaggcattggggagccagcgg 3189 587 707 767 647 printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. 348 tototocattttaaagatgaagaaacaggocgggcacaatggctaatgcctgtaatccca 407 467 768 aagaaaaaaaaaaagatg-----aaacagaggcagaaagactttacgtaaattgctcat 820 Indels 34; Gaps 408 gcactttgggaggctgaggccagaggccagaggtcgcttgagctcagagtttgagaccagcctgg 468 ataacatggcaaaaccctgtctctacaaaaaaaatacaaaaattagatgggtgtggc 528 atgcacctgtggtcccagctacttgggaggctaaggtgggaggatcgcttgagcccaggg 588 agtcaagtctacactgagccatgattggatcactgcactccagcctgggtagacagagca catgtggttgtcaagtttgaccccaaaacccaat------ttattgaccaaggtta ttetttgaetgaggeaagggggteegeteetgggeettgggetttagaaageteatet 3010 taagaaggaacaattggggtttcataactcatgaagagttaaatgagttcaaaagaggga healing; (e) neurological diseases e.g. cerebral anoxia and epile and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the DB 22; Length 23934; musculoskeletal cancers and also for testing and detection e.g. Example 2; SEQ ID NO 2536; 781pp + Sequence Listing; English. Sequence 23934 BP; 7023 A; 4365 C; 4761 G; 7785 T; 0 other; 9.9%; Score 320.4; DB 22; 64.2%; Pred. No. 4.6e-58; live 0; Mismatches 296; Query Match 9.9 Best Local Similarity 64.2 Matches 592; Conservative diagnosis 3070 임 δ qq á g ò Db δ g ò g q ò δŽ

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                       tcaagcgattctcctgcctcagcctc-----ctgagataacaggcgcccgccacac 1102
                                                                                       1103 atctggctaatttttgtatttttagtaaagactgggtttcatcatgttggccaggttggt 1162
                                                                                                                        1163 ttcgaactcctgacctgaggtgagctgcccaccttggcctcccaaagtgctgggattaca 1222
                                                                                                                                3190 tagggactggagagatctg----gaagcataagaaggaatgagacagagtatcactctg 3244
                                                                      3305 tcaagcgattctcatgcctcagcctcccaagtagctgggattacaggcgcatgccacgat 3364
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC,

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Example 2; SEQ ID NO 2544; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyvoiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, inheumatoid atthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. parasitic infections.

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21221 GCAACATGGCGAAACCCCATCTCTACAAAAAATA---CAAAATTAACCAGGTGTTGTGGC 21165
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Pred. No. 4.6e-58;
0; Mismatches 296; Indels 34;
Sequence 23934 BP; 7785 A; 4761 C; 4365 G; 7023 T; 0 other;
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                           Human reproductive system related antigen DNA SEQ ID NO: 7210.
         AAL04522 standard; DNA; 23934 BP
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2000US-0225266.
2000US-0225267.
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                                                                                                                                                                                                                                                                                                                                                                                                   2594 tttctcacataaagaccttacttaggaggccagacgtggtggctcatgcctataatccca 2653
                                                                                                                                                                                                                                                                                                                                                                                                                        2714 gcaacatggcgaaaccccatctctacaaaaata---caaaattaaccaggtgttgtggc 2770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                               tctctccattttaaagatgaagaacaggccgggcacaatggctaatgcctgtaatcca 407
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Pred. No. 4.6e-58;
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           2000US-0256719.

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                                                                                              05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                 protein of the invention.
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3130 attcagagatgaagccagaaggaactctgggttgaggagaaggcattggggagccagcgg 3189
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                                                                                            1163 ttcgaactcctgacctgaggtgagctgccaccttggcctcccaaagtgctgggattaca
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28-JUN-2000;
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19-MAY-2000;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476224/51.

Isolated polypeptide for treating, preventing and, or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis -

Disclosure; SED ID No 777; 546pp; English.

AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU1975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonla, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy.

Sequence 23934 BP; 7785 A; 4761 C; 4365 G; 7023 T; 0 other;

Query Match

9.9%; Score 320.4; DB 22; Length 23934;

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64.2%; Pred. No. 4.6e-58;
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26254.
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08-NOV-2000;
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gcactttgggaggctgaggccagaggatcgcttgagctccagagtttgagaccagcctgg

408

467

2594 tttctcacataaagaccttacttaggaggccagacgtggtggctcatgcctataatccca 2653

348 tetetecattttaaagatgaagaaacaggeegggeacaatggetaatgeetgtaateeea 407

Best Local Similarity 64.2 Matches 592; Conservative

δλ g δ g δ g δλ Q δλ g δy g δ g ŏ

2714 gcaacatggcgaaaccccatctctacaaaaata---caaaattaaccaggtgttgtggc 2770

2771 acatacctgtagtcccagctactgaggaggctgaggcacaagaattgcttgagcctggga 2830

528 atgcacctgtggtcccagctacttgggaggctaaggtgggaggatcgcttgagcccaggg 587

588 agtcaagtctacactgagccatgattggatcactgcactccagcctgggtagacagagca 647

2950 gtagaagtgatcagatatttatctgcataaataaaaaggtagaaagtaattcatattt 3009

768 aagaaaaaaaaaagatg-----aaacagaggcagaaagactttacgtaaattgctcat 820

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccibe production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cexpression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
complement the patients own production of (I). Additionally, (I)
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
concers and cancer metastases of haematopoietic antigen genomic
sequences from the present human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK64703
concerts and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK64703
concerts and cancer metastases of haematopoietic antigen genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 320.4; DB 22; Length 23934;
Pred. No. 4.6e-58;
0; Mismatches 296; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 26254; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23934 BP; 7023 A; 4365 C; 4761 G; 7785 T; 0 other;
                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.9%;
                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                2000US-0251990.
2000US-0254097.
2000US-0251868
                      2000US-0251869
2000US-0251989
                                                                                                               05-JAN-2001; 2001US-0259678
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                   08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
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	1 catgtggttgtcaagtttgaccccaaaacccaatttattgaccaagtta 870				1 ctggcctttctgagatccatccctttctttttttttttt							5 gcctggctaatttttgtattttagtagagacagggttttaccatgttggccaggctgat 3424	3 ttcgaactcctgacctgaggtgagctgccaccttggcctcccaaagtgctgggattaca 1222		3 ggcatgagccactgcgcccagc 1244		
3010 ta	821 ca	3070 ca	871 tt	3130 at	931 ct	3190 ta	991 tc	3245 tc	1051 tc	3305 to	1103 at	3365 gc	1163 tt	3425 ct	1223 gg	3485 gg	
Db	Qy	ОР	Oy	QO	οy	q	Qy	q	Οy	qq	ΟŸ	qq	ΟY	qq	Qγ	qq	

Search completed: September 20, 2002, 03:08:22 Job time: 10571 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- nucleic search, using sw mode] OM nucleic September 19, 2002, 23:25:11; Search time 110.16 Seconds (without alignments) 7204.447 Million cell updates/sec Run on:

1 acagggcatggtggcaggtg.......3ccccacatccccacactt 3231 US-09-846-456-1 Perfect score:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

383533 segs, 122816752 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\* Database

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seg:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seg:\*
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6: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seg:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	<b>\$</b>	DB ID Description	4 US-09-797-906-3 Sequence 3, Appli	3,	3 Sequence 3,	7	12,	20,	21,	22,	Sequence 20,	21 Sequence 21,	-22 Sequence 22,	Sequence 7,	Sequence 3,	Sequence 10,	0 Sequence 10,	-10 Sequence 10,	-43 Sequence 43,	43 Sequence 43,	7 Sequence 17,	Sequence 7, A	5 Sequence 35,	10,	3 Seguence 3,	-095-7 Sequence 7,	3-67 Sequence 67,	
		Length	84495	84495	15297	28720	18073	246240	246240	246240	246240	246240	246240	35060	7680	7210	7210	7210	22481	22481	176373	72604	14796	14796	14796	35060	3507	3507
æ		Match	9.8	8.6	8.4	8.3	8.1		8.0	8.0	7.8	7.8	7.8	7.8	7.8	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4
	Č	Score	278.2	277.2	271.8	269.4	261.6	257.8	257.8	257.8	253	253	253	252.2	251.4	243.4	243.4	243.4	243.4	243.4	243.4	242.4	240.2	240.2	240.2	240	239	239
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Sequence 2, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 3, Appli	Sequence 128, App	Sequence 3, Appli	Sequence 17, Appl	Sequence 7, Appli	Sequence 3, Appli	Sequence 12, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 28, Appl	Sequence 59, Appl	Sequence 8, Appli
US-09-103-875-2	US-08-257-963B-10	US-08-367-841A-10	PCT-US95-07201-10	US-08-367-841A-43	PCT-US95-07201-43	US-08-157-171-3	US-09-050-159-128	US-09-210-748A-3	US-09-128-155-17	US-09-341-587-7	US-09-817-180-3	US-09-078-294-12	US-08-618-100B-3	US-08-973-544-1	US-09-564-805-28	US-09-608-285A-59	US-09-608-285A-8
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4136	7210	7210	7210	22481	22481	1856	1856	7680	176373	28720	15297	18073	10684	5581	26664	15977	9365
7.3	7.2	7.2	7.2	7.2	7.2	7.0	7.0	6.9	6.9	6.9	9.8	6.7	9.9	6.5	6.5	6.4	6.4
234.6	232.6	232.6	232.6	232.6	232.6	226	226	223	222.6	221.8	219.8	217.6	211.8	210.4	209.4	206.6	205.4
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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APPLICATE: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND FITLE OF INVENTION: USES THEREOF FILE REFERENCE: CLOO1151CIP CURRENT APPLICATION NUMBER: US/09/797,906 CURRENT APPLICATION NUMBER: US/09/797,906 CURRENT FILING DATE: 2001-03-05 SOFTWARE: FastSEQ for Windows Version 4.0
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61.5%; Pred. No. 1.1e-58;
tive 0; Mismatches 328;
             Sequence 3, Application US/09797906
Patent No. 6329188
                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

// LCCATION: (1)...(84495)

CHER INFORMATION: n = A.T.C or

US-09-797-906-3
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Best Local Similarity 61.5
Matches 553; Conservative
                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                       LENGTH: 84495
E-906-161-60-SD
                                                                                                                                                                                                                                    SEQ ID NO 3
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TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CLOUISIOL OF COURT OF CURRENT APPLICATION NUMBER: US 009/797,906
CURRENT APPLICATION NUMBER: US 001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                 35170 ccctagatttaatatgtctacaggaaatacaaaggacagagaaacatattaattgacacc 35229
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                                                                                                                                                                             35290 taacaaataatttacgagaaagaaaaagggaggaattcattaaaactggcataagagac 35349
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61.1%; Pred. No. 1.9e-58;
ive 0; Mismatches 338;
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09797906
Patent No. 6329188
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Matches 556; Conservative
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APPLICANT: Zianghe
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GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOI183
CURRENT APPLICATION NUMBER: US/09/817,180
CURRENT FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                   35377 AATAAGGTCTATTGTACTTGATTGCTATGTCTCTTATGCCAGTTTTAATGAATTCCTCCC 35318
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                                                                                                                                 8.4%; Score 271.8; DB 4; Length 15297; 62.9%; Pred. No. 1.8e-57;
                                                                                                                                                                 0; Mismatches 287; Indels
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                   Best Local Similarity 62.98
Matches 577; Conservative
                                                                          ; ORGANISM: Human
US-09-817-180-3
                                             LENGTH: 15297
                                                             TYPE: DNA
                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.3%; Score 269.4; DB 4; Length 28720; Best Local Similarity 61.5%; Pred. No. 9.7e-57; Matches 589; Conservative 0; Mismatches 296; Indels 72;
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APPLICANT: Mollenhauer, Jan
TITLE OF INVENTON: Protein Containing an SRCR Domain
TITLE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                 Sequence 7, Application US/09341587
Patent No. 6346606
                                         Db 15255 ttttaaaaagaatgaag 15271
1258 tttctaagggcaaacag 1274
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fitts, Renee A. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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Db 19639 tatcctcccacctcggcctcccaaagtgctgggattacaggtgtgagccaccatgcc 19695
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62.1%; Pred. No. 6.7e-55;
ive 0; Mismatches 309; Indels 31; Gaps
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Petent No. 6265211
GENERAL INFORMATION
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FLIE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 62.1%
Matches 558; Conservative
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US-09-078-294-12/c
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1258 TCATTATACATTTGTCCAAATCTACAGAATGTACAACACCAAAGCTTGGGTGATAATGAG 1199
1318 AGCAGAGGACTGTCAGGGCAGTCAAATTCTTCTGTATGATACTACAATGGTAGACACATG 1259
                                                                                                                                                                                                                                     1198 GAGTCAATGTTGGTCCATCAATTGCAACAAAGGTACCACAGTGGTGTAGGATGTGGATAA 1139
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                                                          775 aaacaagatgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaa 834
                                                                                                                                                                                835 gtttgaccccaaaacccaatttattgaccaaggttattctttgactgaggcaagggggtc 894
                                                                                                                                                                                                                                                                                                1187 ctgcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgccagc 1244
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APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
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PatentIn Release #1.0, Version #1.30
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ADDRESSEE: TOWNSEND and CREW LLP
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REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 172295 ATAATAATAATAATAATAATAATAATAATAATGGATGCATTTTATCCTATTAATCTTC 172236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 172115 CATGAAGATTATTCTGCATCCATTATTGGTAAGATTGGCCGTTTTCTCCTTTGATCTC 172056
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                                                                                                                                                                                                                                                                                                                                                                                     376 gccgggcacaatggctaatgcctgtaatcccagcactttgggaggctgaggccagaggat 435
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                                                                                                                                                                                                                                                                                                 Score 257.8; DB 2;
Pred. No. 2.1e-53;
0; Mismatches 312;
                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                   STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 246.240 base pairs TYPE: nucleic acid
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Best Local Similarity 61.4%;
Matches 545; Conservative
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Db 172523 CAC-----GAGGTCAAGACCACCCTAGCCGAAATGGTGAAACCCGTCTCTATT- 172473
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Megabase Transcript Map: No. 58 Sequences and Antibodies Thereto
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APPLICATION NUMBER: US/08/724,394A
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61.4%; Pred. No. 2.1e-53;
ive 0; Mismatches 312;
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                                                                                                                                                  Sequence 21, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
                                                                                                                                                                                                                                       Kronmal, Gregory S.
Lauer, Peter M.
Ruddy, David A.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
TRNGTH: 246240 base pairs
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TOPOLOGY: not relevant
DLECULE TYPE: CDNA
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Matches 545; Conservative
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N: 536
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LOCATION: 1..246240
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
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Db 172355 GCCACTGCACTCCAGCCTGGTGACAGAGTGAGACTCCGTCTAAAAATAATAATAATAATA 172296
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556 ggctaaggtgggaggatcgcttgagcccagggagtcaagtctacactgagccatgattgg 615
                                                                                                 796 gaaagactt----tacgtaaattgctcatcatgtggttgtcaagtttgaccccaaaaaccc 851
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                                                                                                                                                                                                     TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
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ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08724394A Patent No. 587237 GENERAL INFORMATION:
APPLICANT: Feder, John N.
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APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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Db 172474 -AAAAATACAAAAGTTAGCTGGCGCGGGGCCACATGCCTGTAGTCCCAGCTACTGGGGA 172416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           796 gaaagactt----tacgtaaattgctcatcatgtggttgtcaagtttgaccccaaaaaccc
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                                                                     PatentIn Release #1.0, Version #1.30
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Pred. No. 2.1e-53;
0; Mismatches 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                017957-000100
                                                                                                                  APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                RECISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFERAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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Best Local Similarity 61.4%;
Matches 545; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 246240 base pairs
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
Floppy disk
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic STRANDEDNESS:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-724-394A-22
                                                                        SOFTWARE:
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Db 171998 GAGACGGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGTGTGTATCTCCGCTCACTG 171939
                                                                                                                                                      Db 171938 CAAGCTCCGCCTCCCGGATTCACGCCATTCTCCTGCCTCAGCCTCCTGAGCAGCTGGGAC 171879
                                                                                                                                                                                                                                                          171878 TACAGGCACCCACCACCACGCCGGCTAATTTTTGTATTTTTAGTAGATACGGGGTTTCA 171819
                                                                                                                                                                                                                                                                                                                                     Db 171818 CTTTGTTAACCAGGATGGTCTCGATCTCCTGACCT--CGTGATGGGCCGCCTCAGCCTC 171761
                                                                                                   taacctctgcctcccgggttcaagcgattctcctgcctcagcctcctga-----gat 1083
                                                                                                                                                                                                       1084 aacaggegccegccaccacatctggctaattttgtatttttagtaaagactgggtttca 1143
                                                                                                                                                                                                                                                                                                             tcatqttggccaggttggtttcgaactcctgacctgaggtgagctgccaccttggcctc 1203
972 gacacggagtcttgctctgtcactcaggctggagtgcagtggcatgatctcgactcactg 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                           171760 CCAAAGTGCTGGGATTACAGGAGTGAGCCACTGCGCCCGGCCCCGTT 171714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Laudr, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-02T-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOWNSEND and TOWNSEND and CREW LLP
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US-08-724-394A-20
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SYSTEM: PC-DOS/MS-DOS
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 01
TELECOMUNICATION INFORMATION: TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
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SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: not relevant
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1..246240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcad
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US-08-724-394A-20
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                                                                                                                                                                                                                                                  DD 171765 CTGAGGCGGGCCGATCA-C-GAGGTCAGAGATCGAGACCATCCTGGTTAACAAAGTGAA 171822
                                                                                                                                                                                                                                                                                                                                                                                 Db 171823 ACCCCGTATCTAC--TAAAAATACAAAATTAGCCGGGCTTGGTGGTGGTGGCTGCCTGTAGT 171880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 171881 CCCAGCTGCTCAGGAGGCTGAGGCAGGAGAATGGCGTGAATCCGGGAGGCGGAGCTTGCA 171940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 172120 AGCCACTTTAATTATGTCTTAAATGAGAGTAACAAATTAAACATAAGAACCTGTAGGGGC 172179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 171705 AAAAAAAAAACGGGGCCGGGCGCAGTGGCTCACTCCTGTAATCCCAGCACTTTGGGAGG 171764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        957 cttttttattttttttgacacggagtcttgctctgtcactcaggctggagtgcagtggcat 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ctgagataacaggcgcccgccaccatctggctaatttttgtatttttagt 1128
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                                                                                                              361 aagatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcactttgggagg 420
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                                                                                                                                                                                                                         421 ctgaggccagaggatcgcttgagctccagagtttgagaccagcctggataacatggcaaa 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                          cccagctacttgggaggctaaggtgggaggatcgcttgagcccagggagtcaagtctaca
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                                                                                                                                                                                                                                                                                                                                 accctgtctctacaaaaaaaatacaaaaattagatgggtgtggtgggcatgcacctgtggt
                                                        30;
Length 246240;
                                                        Indels
  7.8%; Score 253; DB 2; L 61.5%; Pred. No. 3.2e-52; tive 0; Mismatches 315;
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Query Match 7.8%
Best Local Similarity 61.5%
Matches 552; Conservative
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PatentIn Release #1.0, Version #1.30
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CITY: San Francisco
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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APPLICATION NUMBER: US/08/724,394A
FTIING DATE: 01-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David M.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Tra
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
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US-08-724-394A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 171941 GTGAGCGGAGATCACCACTGCACTGGCCTGGGCA-ACAGAGCAAGACTCCGTCTCC 171999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 172000 AAACAACAACAAAAAAAAAAAGGGCAGTGATGTTTATGTGGGTCAGTGTGAAGTAGAGA 172059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 aagatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcactttgggagg 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 253; DB 2; Length 246240; 61.5%; Pred. No. 3.2e-52; live 0; Mismatches 315; Indels 30;
                                                                                    TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                    ADDRESSEE: TOWNSEND and TOWNSEND and CREW STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35,136
ER: 017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFRENCE/DOCKET NUMBER: 0175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                  Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 246240 base pairs
David A.
                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.5'
Matches 552; Conservative
                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01 CLASSIFICATION:
                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                         STATE: CA
                                         APPLICANT:
                                                             APPLICANT:
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Db 172060 TCAAAGGAGAAAACGGCCAATCTTACCAAATAATGGATGCAGAAATAATCTTCATGAGA 172119
                                                                                                                                                         Db 172120 AGCCACTTTAATTATGTCTTAAATGAGAGTAACAAATTAAACATAAGAACCTGTAGGGGC 172179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 172300 ATTATTATTATT-TTTAGACGAGTCTCACTCTGTCAC-CAGGCTGGAGTGCAGTGGCGC 172357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 172478 AGAGACGGGGTTTCACCATTTCGGCTAGGGTGGTCTTGACCTCGTGGTCTG------ 172528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 172358 AATCTCGGCTCGCTGCAACCTCCGCCTCCCGAGTTCAAGCAATTCTCCTGCCTCAGCCTC 172417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 172418 CCCAGTAGCTGGGACTACAGGCATGTGCCACGCCAGCCCAGCTAACTTTTGTATTTTAAT 172477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   957 ctttttattttttttttgacacggagtcttgctctgtcactcaggctggagtgcagtgcat 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ctgagataacaggcgccgccaccacatctggctaatttttgtatttttagt 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatctcgactcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcctc 1076
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                                                                                777 acaagatgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaagt 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 1189 gcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagct 1245
                                                                                                                                                                                                                                         837 ttgaccccaaaacccaatttattgaccaaggttattctttgactgaggcaaggggtccg
                                                                                                                                                                                                                                                                                                              DD 172180 TAAGGGAAAACTTACTCTTTGGCCTCTGAAGAGTCGCTGAAAACCACCGACAAGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                              Megabase Transcript Map: No. 5872237el
Sequences and Antibodies Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 172060 TCAAAGGAGAAAACGGCCAATCTTACCAAATAATGGATGCAGAAATAATCTTCATGGAGA 172119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 172120 AGCCACTTTAATTATGTCTTAAATGAGAGTAACAAATTAAACATAAAGAACCTGTAGGGGC 172179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172180 TAAGGGAAAACTTACTCTTTGGCCTCTGAAGAGTCGCTGAAAACCACCGACAAGAGGAAG 172239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 172000 AAACAACAACAACAAAAAAAACAGGCAGTGATGTTTATGTGGGTCAGTGTGAAGTAGAGA 172059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 172358 AATCTCGGCTCGCTCGCACCTCCCGCTCCCGAGTTCAAGCAATTCTCCTGCCTCAGCCTC 172417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 172418 CCCAGTAGCTGGGACTACAGGCATGTGCCACGCCCCCAGCTAACTTTTGTATT 172477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ctgagataacaggcgcccgccaccacctcggctaattttgtattttagt 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1129 aaagactgggtttcatcatgttggccaggttggtttcgaactcctgacctgaggtgagct 1188
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                                                                                                                                                                                                                                                                                                                                                                                                                           361 aagatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcactttgggagg 420
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                                                                                                                                                                                                                                                                                                                                        Length 246240;
                                                                                                                                                                                                                                                                                                                                   7.8%; Score 253; DB 2; Length 24 61.5%; Pred. No. 3.2e-52; tlve 0; Mismatches 315; Indels
                                                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
                                                                    LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 61.59
Matches 552; Conservative
                                                                                                                                  TOPOLOGY: not rele
MOLECULE TYPE: cDNA
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Db 172529 --CCCGCCTCAGCTCCCAAGTGCTGGGATTACAGGCGTGAGCCATTGCACCCGGCT 172583
                                            1189 goccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagct 1245
Db 172478 AGAGACGGGGTTTCACCATTTCGGCTAGGGTGGTCTTGACCTCGTGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
                                                                                                                                                                                                                                                                             APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ATTI-CHOLINESTERASE SUBSTNACES
CORRESPONDENCE: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTK:.

2 IP: 48334
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEATH PC COMPATIBLE
COMPUTER: PATENT PC TOST MELGASE #1.0, Version #1.30
"TATWARE: PATENT RELEASE #1.0, Version #1.30
"TATON DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter 4089.22464
COCATION: 4089.22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function= "(translation start:
24110)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= "non-translated"
/gene= "ACHE"
/number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cosmid including ACHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Wontgomery, Ilene N.
REGISTRATION NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD: experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: /desc = "Cosmid":
DESCRIPTION:
                                                                                                                                                                                                     Sequence 7, Application US/08814095
Patent No. 6025183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
24090..25177
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OTHER INFORMATION: /fur
OTHER INFORMATION: /ger
OTHER INFORMATION: /num
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Michigan COUNTRY: U.S.
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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OTHER INFORMATION: /number= 7

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NAME/KEY: exon
LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenite resistance
                                                                         NAME/KEY: exon
LOCATION: 25524..26009
LDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
                                                                                                                                                                                                                                                 OTHER INFORMATION: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE" ATURE:
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 27255..28007
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 5
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/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 2
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LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
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RMATION: /gene= "AR"
RMATION: /number= 6
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LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene="AR"
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/number= 1
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                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
28008..28129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        terminator
27385..27387
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LOCATION: 28129..28131
INFORMATION:
INFORMATION:
INFORMATION:
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NAME/KEY:
LOCATION:
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594 gtctacactgagccatgattggatcactgcactccagcctgggtagacagagcaagaccc 653
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7.8%; Score 252.2; DB 3;
Best Local Similarity 58.6%; Pred. No. 2e-52;
Matches 580; Conservative 0; Mismatches 328;
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CTHER INFORMATION: /gene="ARS"
CTHER INFORMATION: /number= 16
US-08-814-095-7
                                                                                                    LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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OTHER INFORMATION: /number= 10
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OTHER INFORMATION: /number= 11
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OTHER INFORMATION: /number= 12
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OTHER INFORMATION: /number= 13
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OTHER INFORMATION: /number= 15
             LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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/number= 14
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OTHER INFORMATION:
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LOCATION: comp.
NAME/KEY: exon
LOCATION: comp
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LOCATION: comp
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                        14296 CTGAATCCATGTTTTTACATAATTGTAGCATCCTTTACACACTCTTCTGTACTTGACTTA 14237
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catgiggitgicaagitigaccccaaaacccaaittatigaccaaggitatici-----
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APPLICANT: Hermeking, Heiko
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REFERENCE: 1107.77810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/210,748A CURRENT FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/069,416
PRIOR FILING DATE: 1997-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13876 CCACACCTGGCCCTCATTCTTTTTT 13848
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1234 etgegeceageteagatecatecetttet 1262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-210-748A-3
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                                                                 5422 atctggccgggcatggtggcttatgcctataatttcagcactttggaaggctgaggcagg 5481
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61.0%; Pred. No. 1.5e-52;
live 0; Mismatches 286; Indels
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; Patent No. 5840686
; GENERAL T.T.T.
  Best Local Similarity 61.09
Matches 575; Conservative
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APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia: Schwartz, Joan P.;
APPLICANT: Patricia: Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PICHENT PATRELUM
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 7.2 kb No. 5840686 1 fragments
OTHER INFORMATION: Derived from human placental genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 7210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMUNICATION INFORMATION:
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                SSEE: Morgan & Finnegan
F: 345 Park Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: DOROTHY R. AUTH
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STRANDEDNESS: Double
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MEDIUM TYPE: Floppy 1
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                                                                                                                                                                                                                        New York
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                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                          10154
                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                        STATE:
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567 gaggatcgcttgagcccagggagtcaagtctacactgagccatgattggatcactgcact 626
                                                                                   807 cgtaaattgctcatcatgtggttgtcaagtttgaccccaaaacccaatttattgaccaag 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08367841A

Patent No. 6319687

GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
ITILE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1216 gattacaggcatgagccactgcgcccagctcagat 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Morgan & Finnegan
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
OTHER INFORMATION: 7.0 kb No. 6319687 1-No. 6319687
OTHER INFORMATION: fragment; Derived from human placental
OTHER INFORMATION: genomic DNA; also referred to as JT106
                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPRAK: (212) 758-4800
TELEFRAK: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
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FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
                                                 FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: JT6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
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tctgtcactcaggctggagtgcagtggcatgatctcgactcactgtaacctctgcctcc 1046
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5915 TATATATCACTTAGGGACAAAAACTTACATGGTAAAAGTAAAAAGAAATGTACGAAAATA 5974
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                                                       5975 ATAAAAATCAAATTCAAGATGGTGGTTATGGTGACGGGAAA-
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Search completed: September 20, 2002, 03:21:22 Job time: 14171 sec

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September 19, 2002, 23:20:20; Search time 3895 Seconds (without alignments) 11196.062 Million cell updates/sec
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3231
1 acagggcatggtggcaggtg......gccccacatccccacctt 3231
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                 Title:
Perfect score:
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IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

27472414 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb\_est2:\*
gb\_htc:\*
gb\_gss:\*
em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* 1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estov:\*
6: em\_estpl:\*
7: em\_estro:\*
8: em\_htc:\*
9: gb\_estl:\* EST:\* 9: 10: 11: 12: 13: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	AU121731	AW748338	AU135588	AW816516	AQ265389	AQ418551	AQ475181	AQ347610	AW023111	AG075934	B50449	AQ537948	AI754653	AQ200209	AV755654	AQ314669	AQ414845	
	DB	6	6	6	σ	12	12	12	12	σ	12	12	12	σ	12	σ	12	12	
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ф	Query	10.4	7.4	6.9	6.8	6.8	6.8	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	
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ORIGIN

AQ040260 CIT-HSP-2 AW341978 hb74d10.x	AQ634562 RPCI-11-4 AW970571 RSTTAB2652	AO587429 CITBI-E1-	AW973181 EST385279	AQ387027 RPCI11-15	BG682030 602629995	AL524675 AL524675	AI733856 zo19c03.y	AW069227 cr41h09.x	AA644090 ab62b04.s	AQ412598 RPCI-11-1	AG102895 Pan troql	BG697612 602660853	AQ221138 HS 2258 B	AV719392 AV719392	AW973187 EST385285	AG050562 Pan trodl	AG036967 Pan trodl	B65075 CIT-HSP-201	B59854 CIT-HSP-345	BG697217 602660451	AI275982 qw06h11.x	AQ426532 CITBI-E1-			
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501 1 416 9	448 1 521 9	575 1				-		-	437 9				477 1	577 9	541 9				642 1	832 1	483 9	490 1	616 1	1750 1	624 1
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## ALIGNMENTS

AU121731 AAMMAI Homo sapiens cDNA clone MAMMA1000851 5', mRNA Sequence. AU121731 AAMMAI Homo sapiens cDNA clone MAMMA1000851 5', mRNA AU121731 GI:10936966 BST. human.	Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 763) 1	153-3 Yana Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@tri.co.jp HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  Location/Qualifiers 1. 763 //Organiam="Homo sapiens" //Clone="MAMMA1000851" //Clone="MAMMA1000851" //Lione_lib="MAMMA1000851"	/
RESULT 1 AU121731 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE OURCE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	BASE COUNT

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, M.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: satupson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=RC6&t2=RC6-BT0252-271099-012-c10&t3=1999-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 146
High quality sequence store: 289.
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RC6-BT0252-271099-012-c10 BT0252 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                            3136 tacttgggcgttattgttttgtttcgaggccaaggaggtttcgggaagtgctcggtttcg 3195
                                                                                                       3076 ggtaggagaaagagacgcaaacacaaaagtggaaaacaggtaagaggctctccagtgact 3135
                                                                                                                                                                                                                                                                                          3016 tttgctccttgttttttccccggttctgttttctccccttctccggaaggcttgtcaagg 3075
                                                                                                                                                                                                                                                                                                                121 TTTGCTCCTTGTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGG 180
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                                                              Gaps
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              Length 763;
                        ; 9.6e-35;
. 9.6e-35;
.hes 0; Indels
              DB 9;
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10.0%; scor.
100.0%; Pred. No. >...
0; Mismatches
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         Query Match
Best Local Similarity 100.C
Matches 336; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue many and conn amplification were performed under low
                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 24-0CT-2000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1538-3-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                     2006 getgeaettcacaaatgtatacaaactaaatacaagteetgtgtttttateacagggagg 2065
                                                                                                                                                                                                                                                                                                                                                                                 2126 tigittigittgittttttttgittttigiggoctoottoototoaittaigaagaga 2185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU135588 PLACEI Homo sapiens CDNA clone PLACE1002437 5', mRNA
                                                                                                                                                                                                                         Length 289;
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                                                                                                                                                                                                                      7.4%; Score 237.8; DB 9; 92.3%; Pred. No. 8.6e-22; ative 0; Mismatches 12;
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                                                                                                                              stringency conditions."
70 c 51 q 7
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/clone_lib="PLACE1"
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Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                               Query Match 7.49
Best Local Similarity 92.33
Matches 276; Conservative
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 457)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costaf,F.F.,
Oldman,G.H., Carvalho,A.F., Matsukuma,A. Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV0-ST0236-171 Seq primer: puc 18 forward High quality sequence stop: 457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                        2894 gtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctc 2953
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                                                                       Length 736;
 others
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                                                                     6.9%; Score 221.8; DB 9 99.1%; Pred. No. 6.8e-20; Live 0; Mismatches 2
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170
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/db_xref="taxon:9606"
/clone_lib="ST0236"
/dev_stage="Adult"
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                                                                                       Best Local Similarity 99.1
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CITBI-E1-2509010.TF CITBI-E1 Homo sapiens genomic clone 2509010,
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
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Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       taaagactgggtttcatcatcatgttggccaggttggtttcgaactcctgacctgaggtgagc 1187
                                                                                                                                                                                                         955 ttctttttatttttcttgacacggagtcttgctctgtcactcaggctggagtgcagtggc 1014
                                                                                                                                                                                                                                                                                             tcctga----gataacaggcgccgccacacatctggctaatttttgtatttttag 1127
                                                                                                                                                                                                                                 277 TAGAGACGGGGTTTCACCACGTTGGCCACGCTGGTCTCGAACTCCTGACCTCAGGTGATC 218
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                                                                                                                                                                Gaps
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Other_GSSs: CITBI-E1-2509010.TR
Other_GSSs: CITBI-E1-2509010.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
FEX: 301 838 0208
                                                                                                                                                           38;
                                                                                                                   DB 9;
                                                                                                                Score 221.2; DB Pred. No. 1e-19;
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/clone_lib="CITBI-E1"
/sex="male"
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/db_xref="GDB:7577811"
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Homo sapiens genomic clone RPCI-11-203K4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Pieter de Jong Pieterde de Jong Pieterdedejong, med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seq primer: SP6 class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 544)
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
127 c 137 g 146 t
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                                                                                                                                                                                                   1016 tgatctcgactcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcct 1075
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Fax: 301 838 0208
Email: bhe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                   8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 GAGATACATTTTTGTAAATCTAGACTGGAGGTCAGTGGACAGCTCCTCAGGCAAAGGGAG 72
                                                                                                                                  DB 12; Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                              Score 219.4; DB 12; Length
Pred. No. 1.6e-19;
0; Mismatches 71; Indels
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Other_GSSs: RPCI-11-203K4.TV
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DNA sequence.
AQ418551
AQ418551.1 GI:4476275
                                                                                                                                6.8%;
                                                                                                                            Query Match
Best Local Similarity 78.0%
Matches 280; Conservative
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KEYWORDS
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AQ418551
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from Callech Libraries for Sequence-Ready
Map Building
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CITBI-E1-2589B9.TF CITBI-E1 Homo sapiens genomic clone 2589B9, DNA
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                                                                                     /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                    ttgggaggctgaggccagaggatcgcttgagctccagagtttgagaccagcctggataac 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 cctgtgggtcccagctacttgggaggctaaggtgggaggatcgcttgagcccagggagtca 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 ccattttaaagatgaagaaacaggccgggcacaatggctaatgcctgtaatcccagcact 412
                                                                                                                                                                                                                                                                                                                                                                                           81 CCATTAGAAATAAAGGAAGAGCGGCCAGGAGTAGTGGCTCATGCCTGTAATTGCAGCACT 140
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
                                                                                                                                                                                                                                                     Score 218.6; DB 12; Length 544;
Pred. No. 2e-19;
0; Mismatches 125; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other GSSs: CITBL-E1-258989.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
                                                                                                                                                             1 others
                                                                                                                                                             85 t
              /clone="RPCI-11-203K4"
/clone_lib="RPCI-11"
/sex="Male"
/db_xref="taxon:9606
                                                                                                                                                             165 g
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                                                                                                                                                                                                                                                       Query Match 6.8%;
Best Local Similarity 70.5%;
Matches 306; Conservative C
                                                                                                                                                             86 c
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human.
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Best Local S
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RPCI11-126022.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-126022,
DNA sequence.
                                                                                                                                                                                                                                                                                                              ij
        Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)
                                                                                                                                                                                     /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
162 c 180 g 149 t
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                                                                                                                                                                                                                                                                                                             83; Indels
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                                                                                       Location/Qualifiers
1. 719
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                              /clone="2589B9"
/clone_lib="CITBI-E1"
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Other_GSSs: RPCI11-126022.TV
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                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                              Matches 283; Conservative
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Fax: 301 838 0208
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Best Local Similarity
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df49d08.yl Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486822 5', mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 338)
Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R.
                                                                                                                                       Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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8
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                      MD 20850
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                                                                      9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7548357"
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/clone="RPCI-11-126022"
/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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AG075934.1 GI:16627736
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-068P19.R.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                  Eljiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanasee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was generated during the R&D process and may have higher chance of
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Fullyman.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totocki,Y., Mattanabbe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Pred. No. 8.8e-19;
0; Mismatches 136; Indels
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Best Local Similarity 69.7%;
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/db_xref="taxon:9606"
/clone="IMAGE:12486822"
/clone="IMAGE:12486822"
/clone="IMAGE:12486822"
/clone="Lib="Morton Fetal Cochlea"
/dev_stage="lb="2"
/dev_stage=
and Morton, C.C.
Isolation of novel and known genes from a human fetal cochlear CDNA
lbrary using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                        DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LLAM6188 row: G column: 15
Seq primer: MISR21 reverse primer (ABI).
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Pan troglodytes DNA, clone: PTB-068P19.R, genomic survey sequence.
                                                                                                                                                                                                            Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 738 6996
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                                                                                                                                                                                                                                                                                                                                                                  Email: ccmorton@bics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                      Contact: Morton, C.
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                                                             332 CGCCCGGCCCTCAGCTTTCAAATGACAA 365
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/sex="Male"
/cell_type="Lymphocytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                             Kim, U.-J., Adams, M.D. and Simon, M.I.
Determination of clone end sequences of human Bacterial Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gaps
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Division of Biology, MS 147-75, Pasadena, CA 91125,
15 (26 796 706)
Fax: 626 395 4901
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/organism="Homo sapiens"
/db_xref="GDB:5393148"
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Other_GSSs: CIT-HSP-422022.TP
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/clone_lib="CIT-HSP"
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                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Ung-Jin Kim
CalTech Genome Research Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 622)
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178 c 103 g 218 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hbe@tigr.org
Clones are derived from the human BAC_library RPCI-11. For BAC
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
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950 tccctttcttttatttttcttgacacggagtcttgctcgtcactcaggctggagtgca 1009
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/db_xref="GDB:7517234"
/db_xref="taxon:9606"
/clone="RPCI-11-4503"
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/cell_type="Lymphocytes"
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1 (bases I to 514)

13a,L.B., Young,M.; Touchman,J.W., Bouffard,G.G.,
Beckstrom-Sternberg,S.W., Green,E.D., Powell,J.I., Yang,L.M., Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.
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/lab_host="XLI-Blue MRF'/SOLR"
/note="Vector: pRluescript, Site_1: EcoRI; Site_2: XhoI;
mRNA made from human bone marrow stroma, cDNA made by
oligo-dT priming. Directionally cloned. Size-selected for
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                                                  601 ctgagccatgattggatcactgcactccagcctgggtagacagagcaagaccctgtctca 660
                                                                                  222 GIGAGCCAAGATCATGCCACTGCATTCCAGCCTTGGT-GACAGAATAAGACCCTGTCTTA 164
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Plate: 28 row: c column: 08
Seq primer: -21M13 forward primer (ABI).

Location/Qualifiers
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10/100101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
TEL: 301-402-4877
Fax: 301-496-7157
                                                                                                                                                                                  6.6%; Score 213; DB 9; Length 514;
81.8%; Pred. No. 1.1e-18;
tive 0; Mismatches 50; Indels
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/sex="mixed"
/tissue_type="bone marrow stroma"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Libin Jia
Medical Genetics Branch
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139 c 1
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nes 261; Conservative
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other_GSSs: RPCIII-4503.TK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1074 ctcctga-----gataacaggcgcccgccacatctggctaattttgtatttt 1125
                                                                                                                                      1126 agtaaagactgggtttcatcatgttggccaggttggtttcgaactcctgacctgaggtga 1185
                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"
174 c 182 q 170 t
                                                                       134 CTCCTGAGTAGCTGGGATTACAGGCGCGCCACCACCACGCCCGGCTAATTTTTGTATTTTT 193
                                                                                                                                                                                                                                                                                                                             254 TCCGCCTCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACTGCGCCCAGCC 313
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Clones are derived from the human BAC library RPCI-11. For BAC
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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309 CGIGAICTIGGCICACIGCAACCICIGCACCGGGTICAAGCGAITITCCIGCCICAGC 250

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 827)

8 Gu,J., Zhao,M., Huang,O., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,

8 Gu,J., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Zuog,

L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,

Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.,

Nor apiens CDNA BM clones

Nor apiens CDNA BM clones

Contact: Zequang Ham

Contact: Zequang Ham

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801919

Fax: 86-21-50801919

Fax: 86-21-50801922

Email: hanzgenge.Sh.cn

This clone is available at CHGC in Shanghai.
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Best Local Similarity 84.2%; Pred. No. 9e-19;
Matches 255; Conservative 0; Mismatches 40; Indels 8; Gaps
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/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
                                                                                                                                                                                                  AV/55654 BM Homo sapiens cDNA clone BMFBHD03 5', mRNA sequence AV755654
536 TICTITITITITITITITITIGAGACAGACTCTCCCTCTGTCACCCAGGCTGGAGTGCA 477
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/db_xref="taxon:9606"
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/clone_lib="BM"
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## SUMMARIES

Description Query Score Match Length DB, ID Result

AX351030 Sequence AE275948 Homo sapi AX092589 Sequence AJ552277 Homo sapi AL35365 Human DNA AC012230 Homo sapi AF287262 Homo sapi AC021345 Homo sapi AC021345 Homo sapi AX060713 Sequence AX06092 Sequence AX06092 Sequence AX060719 Sequence	AXO60721 Sequence AXO60908 Sequence AX35103 Sequence AX258627 Homo sapi AX12764 Sequence AX13751 Sequence AX12751 Sequence AX12763 Sequence AX12703 Sequence AX1371 Sequence AX1371 Sequence AX1371 Sequence AX1371 Sequence AX1371 Sequence AX135103 Sequence AX35103 Sequence AX3510	DNA linear PAT 06-FEB-2002  6.  raniata; Vertebrata; Euteleostomi; atarrhin; Hominidae; Homo. Lemoine,C., Naudin,L., Denefle,P., 'A. and Santamarina-Fojo,S. :es of the abcl gene :001;
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Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Ereeman,L., Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C., Prades,C., Chinini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A., Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E., Francois,T.L. and Brewer,H.B. Jr.
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Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
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PCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW
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PAT 21-MAR-2001 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183999)
1 (bases 1 to 183999)
Compositions and methods for modulating hdl cholesterol and triglyceride levels
Patent: Wo 0115676-A 1 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA) Length 183999; 386 others linear Query Match 98.4%; Score 351.2; DB 6; Best Local Similarity 98.9%; Pred. No. 3.2e-96; Matches 353; Conservative 0; Mismatches 4; DNA 1. .183999 /organtism="HOmo sapiens" /db\_xref="taxon:9606" 49549 a 37944 c 41170 g 54950 t 183999 bp Sequence 1 from Patent W00115676. AX092589 AX092589.1 GI:13444647 human. DEFINITION ACCESSION VERSION KEYWORDS SOURCE BASE COUNT ORIGIN ORGANISM AUTHORS TITLE JOURNAL REFERENCE AX092589 FEATURES Locus

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Gaps

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Indels

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PRI 08-JAN-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
                                                                                                                                                                                      53309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-JAN-2000) Porsch-Oezcueruemez M.K., Institute for Clinical Chemistry, University of Regensburg, Franz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porsch-Oezcueruemez, M., Langmann, T. and Schmitz, G. Cloning and Characterization of the human ATP-binding Cassette Transporter-1 (ABC-1) Promoter
                                                             ataactgatggctgtttcccctcctgctttatctttcagttaatgaccagccacggggt 120
                                                                                                                                                                                                                                                     241 ttcagaagaagaagacaaacagtaagcttgggtttttcagcagcggggggttctctctatttt 300
                                                                                                                                                                                                                                                                                                                                    ccttgctgtcagctctggccgctgccttccagggctcccgagccacacgctgggcgtgct
                                                                                                                                           'Tunction="cholesterol efflux regulatory proteiin"
1 tggaggtctcagctgagagggctggattagcagtcctcattggtgtatggctttgcagca
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/product="Arp-binding cassette transporter-1"
/protein_id="CA021428_1"
/db_xref="G1:12140345"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABC-1 gene; ATP-binding cassette transporter-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MACWPQLRLLLWKNLTFRRRQT"
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/db_xref="taxon:9606"
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/cell_type="leukocyte"
189. 346
/gene="ABC-1"
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Porsch-Oezcueruemez, M.K.
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'gene="ABC-1"
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEPP; Information on the WORMPEPP database can be found at
                                                     ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL353685 129608 bp DNA linear PRI 01-JUN-2001
Human DNA sequence from clone RP11-31J20 on chromosome 9, complete
sequence.
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On Jun 8, 2001 this sequence version replaced gi:14272260.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annoctated as variations together with a note of the overlapping clone variation annotation may not be found in the sequence submission
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RP11-31J20 is from the library RPCI-11.1 constructed by the group
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                90 TGGAGGTCTCAGCTGAGAGGGCTGGATTAGCAGTCCTCATTGGTGTATGGCTTTGCAGCA 149
                                                                                                                                                                                                                                                                                                                          121 occtgotgtcagotctggccgctgccttccagggctcccgagccacacgctgggcgtgct 180
                                                                                                                                                                                                                                                                                                                                                                                268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 TICAGAAGAAGACAAACAGIAAGCIIIGGGIIITIICAGCAGCGGGGGGTICICICATIIII 388
                                                        Gaps
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                                                                                                              1 tggaggtctcagctgagagggctggattagcagtcctcattggtgtgtatggctttgcagca
                                                                                                                                                                                                                                                                       150 ATAACTGATGGCTGTTTCCCCTCCTGCTTTATCTTTCAGTTAATGACCAGCCAC-GGCGT
                                                                                                                                                                                                                                                                                                                                                          209 CCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCT
                                                        1;
Length 480;
                                                        Indels
  DB 9;
  Score 340.2; DB 9
Pred. No. 2.9e-93;
0; Mismatches 3
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  95.3%;
98.9%;
                                                        Conservative
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AL353685.23
  Query Match
Best Local Similarity
Matches 353; Conserv
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IMPORTANT: This sequence is not the entire insert of clone RP11-31J20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-31J20 is at 129608 in this sequence. The true right end of clone RP11-413C10 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6522. .6818
//Ancte="Aluga repeat: matches 1. .295 of consensus"
7282. .7415
//Ancte="LiMb8 repeat: matches 6040. .6173 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // 16105. .161044
// note="10 copies 4 mer caca 100% conserved"
// note="10 copies 4 mer caca 100% conserved"
// note="11704]
// note="Milks repeat: matches 64. .246 of consensus"
// note="Alusg repeat: matches 1. .287 of consensus"
// note="Alusg repeat: matches 1. .293 of consensus"
// note="Alusg repeat: matches 1. .293 of consensus"
// note="Milks repeat: matches 1. .308 of consensus"
// note="Milks repeat: matches 49. .212 of consensus"
// note="Milks repeat: matches 7. .302 of consensus"
// note="Alusx repeat: matches 7. .302 of consensus"
// note="Alusx repeat: matches 10. .146 of consensus"
// note="Milks repeat: matches 10. .307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23427. .2345

// note="L2 repeat: matches 2137. .2750 of consensus" 24245. .24544

// note="Alusg repeat: matches 2. .302 of consensus" 24556. .24587

// note="8 copies 4 mer acac 96% conserved" 26551

// note="29 copies 2 mer ta 69% conserved" 26849. .26892

// note="11 copies 4 mer tata 81% conserved" 26849. .26892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8145. 8434
Anote="AluSc repeat: matches 1. .298 of consensus" 1.2745. 1.2713
Anote="L2 repeat: matches 1363. .1940 of consensus" 1.3890. .13969
Anote="L2 repeat: matches 2611. .2701 of consensus" 1.3890. .1541
Anote="16 copies 2 mer ac 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="L2 repeat: matches 2649. .2698 of consensus"
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/note="AluSc repeat: matches 1. .288 of consensus"
1828. .1877
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/note="MIR repeat: matches 12. .250 of consensus"
2777. _2896
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27998. .28103
/note="WIR repeat: matches 28. .145 of consensus"
28515. .28626
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28986. .29213
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of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                            Location/Qualifiers
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/note="LIMD2 repeat: matches 5774. .6331 of consensus" 40256. .40534
40206. .2533 of consensus" 41476. .416155
                                                                                                                                                                                                                                                                                                      // Josephson State A mer atgg 79% conserved" 34435...34588 | Angle A mer atgg 79% conserved" 34435...34588 | Angle A metches 13...189 of consensus" 34729...34873 | Anote="MIR repeat: matches 77...198 of consensus" 35802...3591 | Anote="2 copies 39 mer 92% conserved" 37613...37980
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/note="LiMA9 repeat: matches 5893. .6307 of consensus"
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49097. .49181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Min repeat: matches 30. .185 of consensus" 42010. .42194
/note="Min repeat: matches 49. .234 of consensus" 44099. .45239
/note="Tirloh repeat: matches 6. .450 of consensus" 45359. .45486
                                                                                                                                                Anote-"WERSA repeat: matches 60. .188 of consensus" 32450. .32536
Anote-"WERSA repeat: matches 14. .106 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56750. 56889 From matches 2565. 2710 of consensus 77406. 57567 repeat: matches 4. .187 of consensus 700te="MER5A repeat: matches 4. .187 of consensus"
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49578, .49758
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/note="MIR repeat: matches 20. .183 of consensus"
                                  31424. .31734
/note="AluSp repeat: matches 1. .308 of consensus"
31987. .32116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSc repeat: matches 1. .308 of consensus" 39674. .40243
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54337. .54544
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17915. .48083
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/note="MIR repeat: matches 25. .246 of consensus"
54754. .55032
/note="AluSp repeat: matches 1. .302 of consensus"
55042. .55343
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/note="AluSg repeat: matches 1. .302 of consensus"
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/note="10 copies 4 mer acac 97% conserved" 47118. .47429
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51677. .51977
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="MER5A repeat: matches 72. .186 of consensus"
66825. .67131
           /note="MiR repeat: matches 78. .243 of consensus" 6459. .6453 mote="32 copies 2 mer ta 70% conserved" 64593. .64656 /note="16 copies 4 mer atat 68% conserved" 64981. .65042 /note="MERSA repeat: matches 15. .72 of consensus" 65043. .65341 /note="Alux repeat: matches 1. .299 of consensus"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Submitted (21-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 22, 2000 this sequence version replaced gi:6454033. All repeats were identified using RepeatMasker:
                                                                                                                                                      Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zlmmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator B1g Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 117571 bases at least Q40 Consensus quality: 145749 bases at least Q30 Consensus quality: 160940 bases at least Q20 Insert size: 185000; agarose-fp Insert size: 171264; sum-of-contigs Quality coverage: 2.9 in Q20 bases; sum-of-contigs Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5885: gap of 100 bp
7879: contig of 1994 bp in length
7979: gap of 100 bp
9686: contig of 1707 bp in length
9786: gap of 100 bp
12253: contig of 2467 bp in length
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2735 4415: contig of 1681 bp in length
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28184: contig of 2377 bp in length
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38318: contig of 3919 bp in length
                                                                                                                                                                                                                                                 Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                      Center project name: L2510
Center clone name: 1_M_10
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20131: cont
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13182 138059; config of 6678 bp in length 138060 138159; gap of 100 bp 138160 145491; contig of 7332 bp in length 145592 157391; contig of 11800 bp in length 15732 157491; gap of 100 bp 157392 157491; gap of 100 bp 157492 157491; gap of 100 bp 157492 175064; contig of 17573 bp in length 157492 175064; contig of 17573 bp in length.
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                         48216: gap of 100 bp
52618: contig of 4402 bp in length
                                                                                                                                                                                                           135: gap of 100 bp
63661: contig of 3926 bp in length
61: gap of 100 bp
68437: contig of 4676 bp in length
                                                                                          p of 100 bp contig of 3874 bp in length
                                                                                                                                                    p of 100 bp contig of 2943 bp in length
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76888: contig of 5330 bp in length
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1. .1003
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/note="assembly_fragment"
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48116: contig of
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                                                                                                                                              092: gap of
59635: con+
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41: gap of

68437: ~
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                                                                                    52718: gap of 56592: cont
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97901; cont
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Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1) and SNAP protein genes, complete cds.

AF287262.1 GI:13876612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20114)
Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F.
Human and mouse abcal comparative sequencing and transgenesis
studies revealing novel regulatory sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151451 ATAACTGATGGCTGTTTCCCCTCCTGCTTTATCTTTCAGTTAATGACCAGCCAC-GGCGT 151393
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                                                                                                           42936. .45448
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31439. .34299
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71559. .76888
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VERSION
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AUTHORS
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SOURCE
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MEDLINE REFERENCE

JOURNAL

AUTHORS JOURNAL mRNA

FEATURES

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join(33931. 379049;101048. 101169;104122. 104328,17520. 77661,
78931. 79049;101048. 101169;104122. 104328,117287. 117379,
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130079. 1303703. 131228,131749. 131925,
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153438. 15535,15658. 156429,165417. 162491,
163013. 163182,164413. 164590;16588. 166703,
166815. 16692,171017. 171079;171997. 172093,
174448. 174589;174961. 175095;176039. 176442,
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QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN
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NKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQOMPY
PCYVDDIFLRVWSRSMPLFWTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW
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                                                                             Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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    201144
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Genomics 73 (1), 66-76 (2001) 21251004
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SOLSGOMORKLSVALEVGGSKVVILDEPTAGVDPYSRGIMELLIKYRGGRTIILST
HHMDEADVLGDRIAIISHGKLCCVGSSLFLKNOLGTGYYLTLVKKDVESSLSSCRNS
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DAIKQMKKHLKLAKDSSADRFLNSLGREWTGLDTRNNVKWWRNNKGHAISSFLNVIN
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MDPKARRFLMNCALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLK
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exon

/gene="ABCAl'

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S Birren, B. Lintcon, L. Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Lintcon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Bernah, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhudh, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., Fitzhudh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, R., Peirani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Perre, N., Peisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Perre, M., Peterson, R., Peter
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Direct Submission

Besearch, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:6705761.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This record contains 92 individual

* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L4483
Center clone name: 24_J_9
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if 905 bp in length
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911 1010: gap of 100 bp
1011 1873: contig of 863 bp in length
1874 1973: gap of 100 bp
1974 2824: contig of 851 bp in length
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of 883 bp in length
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if 878 bp in length
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Unpublished
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3802: contig of 8
3 3902: gap of 100
4816: contig of 9
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1874 1973; gap of
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                     AC021345.
AC021345.2 GI:9130845
HTG; HTGS_PHASE0.
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  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 201144;
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Pred. No. 7.7e-93;
0; Mismatches 3
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/number=31
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150280. .150428
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/gene="ABCA1"
                       140179. .140350
/gene="ABCA1"
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142777. .142919
                                                                                                                                                                                                                                                                                                                              143963. .144183
/gene="ABCA1"
                                                                                                                                                                                                                                                                                                                                                                                     /number=23
145441. .145513
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/gene="ABCA1"
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/gene="ABCA1"
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152078. .15
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143963. .14
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                                                                                                                                                                                                                                 number=21
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Best Local Similarity 98.99
Matches 353; Conservative
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8755: contig of 908 bp in lengtn
5: gap of 100 bp
9753: contig of 898 bp in length
3: gap of 100 bp
10757: contig of 904 bp in length
                                                                                                                                                                                                                                                                                                            1371 13810; gap of 100 bp 100 bp 101 length 14685 14784; gap of 100 bp 14685 14784; gap of 100 bp 15662; contig of 878 bp in length 15662; contig of 878 bp in length 15663 15662; contig of 915 bp in length 15763 16677; contig of 915 bp in length 15763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25521: contig of 867 bp in length 121: contig of 867 bp in length 122: 25487: contig of 866 bp in length 187: gap of 100 bp 100 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52: gap of 100 pp
16677: contig of 915 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17778: gap of 100 bp
18679: contig of 901 bp in length
18779: gap of 100 bp
19632: contig of 853 bp in length
19732: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20734: gap of 100 bp 21620: contig of 886 bp in length 21720: gap of 100 bp 22579: contig of 859 bp in length
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38502: gap of 100 bp

39380: contig of 878 bp in length

39480: gap of 100 bp

40407: contig of 927 bp in length
                                                                                                                                                   10857; gap of 100 bp 11732; contig of 875 bp in length 11832; gap of 100 bp in length 12739; contig of 907 bp in length
                                                                                                                                                                                                                                                                  39: gap of 100 bp
13710: contig of 871 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16777: gap of 100 bp
17678: contig of 901 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19732: gap of 100 bp
20634: contig of 902 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22679: gap of 100 bp
22568: contig of 889 bp in length
23668: gap of 100 bp
24554: contig of 886 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27564: gap of 100 bp
28466: contig of 902 bp in length
28566: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30547; gap of 100 bp 13153; contig of 906 bp in length 13153; gap of 100 bp 23452; contig of 899 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34535: gap of 100 bp
35433: contig of 898 bp in length
35533: gap of 100 bp
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99: contig of 858 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29564: gap of 100 bp
30447: contig of 883 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32552: gap of 100 bp
33447: contig of 895 bp in length
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44356: contig of 899 bp in length
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contig of 908 bp
of 100 hr
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.v: gap of
40407: ~
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42399: conf
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10857:
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11733
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61 ataactgatggctgtttcccctcctgctttatctttcagttaatgaccagccacggggt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 50350; gap of 100 bp in tength 15120; contig of 859 bp in length 15130; gap of 100 bp 25221; contig of 859 bp in length 25221; gap of 100 bp 25235; contig of 884 bp in length 165305; gap of 100 bp 25205; contig of 884 bp in length 165305; gap of 100 bp 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 5724; gap of 100 bp 122 58121: contig of 897 bp in length 22 58121: contig of 897 bp in length 22 59175; gap of 100 bp 100 bp 10058; contig of 883 bp in length 100 bp 10058; contig of 883 bp in length 100 bp 1
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904 bp in length
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           in length
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                                                                                                                                                                                                                                                         3 47402: gap of 100 bp 48293: contig of 891 bp in 48293: gap of 100 bp 49280: contig of 887 bp in 1 49380: gap of 100 bp 1 50250: contig of 870 bp in
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Pred. No. 1.3e-65;
0; Mismatches 4
45325: contig of 869 bp ir
425: gap of 100 bp
44305: contig of 880 bp ir
405: gap of 100 bp
47302: contig of 897 bp ir
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4: gap of
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2025) 1 (2
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Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene, exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200)
Pullinger, C.R., Hakamata H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hARCI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
Blochem. Blophys. Res. Commun. 271 (2000) In press
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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AX060713
AX060713.1 GI:12406103
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/db_xref="taxon:9606"
/chromosome="9"
/map="9q31"
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abcl polypeptides Patent: Wo 0070871-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
                                                                                                                             97 cagttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggct 156
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Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, complete cds. AF285167.1 GI:9755158
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KEKLAABENULKAN DILKPILATUNTSEPEKELAERIKULUGE VELLOGIE
SWEDBRAGEVBELTANNSSESSTOJ YOAVSR TVGHEBGGGLK IKSLAWY EDNBYK ALF
GGGTEEEDAEFFYDNSTFPYCNDLMKNLESSPLSR IIWKALKPLLVGELTFPPTPAT
RQVMARVNKTFPOLELAYTHDLEGMWEELSPK IWTFWENSOEMDLVRALLDSRDNDHFWE
QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSYYTWREAFNENDATHYKYK TRADIDOVPRT
NKIED TATEWWILNKSMELLEBKR WAGGSTYTTPGSIELEPHHYKYK TRADIDOVPRT
NKIKDGYWDFGPRANNYWGGPAYLQDVVEQAIIRVITTGTEKKTGYWQOMPY
PCYVDDIFLRVMSRSWPLFMTLAWIYSVAVIIKGIVYEKEARLKETMRINGLDNSILM
SRFISSLI IPLLVSAGLLVYIKLGMILPSEDSVVEVELESVRAVYTLGGFLISTLE
EQGIGVQWDNLFESPVEEDGFNITTSISMALFYSTKKTGYRAVGOPF
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ARLFSDARRLLLYSOKDTSMKDMRKVLRTLQOIKKSSSNLKLODFLYDNETFSGFLYH
NLSLPKSTYDKMLRADVILHKVFLOGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
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AVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIR
ONLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKT
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DGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                           255 CCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGG 314
                                                        217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
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Lawn, Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Direct Submission
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/protein_id="AAF98175.1"
/db_xref="GI:9755159"
                                                                                                                                                                                                                  375 GTGGCCTGGCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGG 419
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/organism="Homo sapiens"
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/cell_type="fibroblast"
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GWKLTQQQEYALLWKRLLIARRSKRGFFAQIVLPAVEYCIALYFSLIVPPEGKYPSLE
LQPWMYNEQYTFVSNDAPEDTGTLELLAALTKDPGFGTRCMEGNPIPDTPCQAGEEEW
TTAAYPQTIALLEGNGNWTWQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKONTA
DILQDLTGRNISDYLWKTYQIIARSLKNK WWNERRYGGFGLYSWYQALPPEQRKONTA
DIIKQMKKHLKLAKDSSADRFLNSLGREWTGLDTRNNYKWFNNKGWHAISSFLNVIN
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NAILKANLQKGENSHYGTTAFNHPLNLTKQQLSFYALMTSYDVLYSICVIFMSFY
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TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDWYKNQAMADALERFGENRFYS
PLSNGLYGRNZFRYRKRRPANDRICGTLGRGSVA
TFVLELFTDNKLNINDILKSVFLIFPHFCLGRGLIDWYKNQAMADALERFGENRFYS
PLSNGLYGRALFANNSCOWPLIFFUNDUNGYCPOFDAITELLTGREHVEFFALLRGV
RILDGGGONDILETKELTKTTRRKRRPANDNICGTPPTGRENVEFFALLRGV
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RDPKARRFLWNCALSVVKGGRSVLTSNIHEVHONMGYCPOFDAITELLTGREHVEFFALLRGV
NREGDGYTIVVRIAGSNPDLKFVQDFFGLAFFGSSLARI
FSILSQCKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNUZYQLPSSLSSLARI
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Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abcl Patent: Wo 00708972-A 7 28-DEC-2000; CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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81.8%; Pred. No. 1.2e-37;
Live 0; Mismatches 41;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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217 ttgctgctgtggaagaacctcactttcagaagaagaagacaacagtaagcttgggttttca 276
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abc1 polypeptides
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81.8%; Pred. No. 1.2e-37;
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Sequence 9 from Patent W00078972.
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Patent: WO 0078971-A 7 28-DEC-2000;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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2000US-0213958.
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WO200115676-A2.
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Treating a lower than normal high density lipoprotein-cholesterol

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ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
                                                                                                                 The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCl expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Nomann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 53130 tggaggtctcagctgagagggctggattagcagtcctcattggtgtatggctttgcagca 53189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctcact 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ataactgatggctgtttcccctcctgctttatctttcagttaatgaccagccacgggcgt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ccctgctgtcagctctggccgctgccttccagggctcccgagccacacgctgggcgtgct 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 183999
                                                                                                                                                                                                                                                                                                                                                                                      98.9%; Score 351.2; DB 22; Lenyc... 98.9%; Pred. No. 1.3e-97; ... "**cmatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ABC1 gene exon 1 (promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC69132 standard; DNA; 10545 BP.
                                                                                 Claim 8; Fig 1; 317pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.93
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000.
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The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is cocated on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (High density lipoprotein) deficiency (HAA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while the inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, coronary restencess, and peripheral vascular disease.

Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention promprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease compounds which mimic ABC1 activity, one or second and methods for determining whether a patient has an increased risk for cardiovascular disease compounds which mimic ABC1 activity, one compasses compounds which mimic ABC1 activity, one or second or stimulate ABC1 expression and methods of screening for such compounds with interaction or prevent cardiovascular disease, especially coronary artery disease, or prevent cardiovascular disease, especially coronary artery disease, corporascular disease, sepecially coronary artery disease, corporascular disease, sepecially soronary actenosis or peripheral vascular disease, which as alzheimer's disease, which acceptive soronary selectoris soronary actery disease, with ABC1 bloological activity, such as Alzheimer's disease, with annothing or or prevent cardiovascular disease. They may also b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention specifically excludes proteins with the exact amino acid sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as Genbank Accession No: AJ012376.1. The present sequence represents the human ABCl gene promoter region (exon 1).
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                                                                                                                                                                                                                                                                                                                                                           New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                      Hayden MR, Wilson AR, Pimstone SN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 50; Fig 12; 229pp; English.
                                                                                                                                                                                                                       (XENO-) XENON BIORESEARCH INC
                                                                                                                                                                                                (UYBR-) UNIV BRITISH COLUMBIA
                    15-MAR-2000; 2000WO-IB00532.
                                                                   99US-0124702.
                                                                                             99US-0138048.
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Best Local Similarity 98.99
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            disease and cancer -
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                                                                                             08-JUN-1999;
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are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for
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                                                                                                                                                                                                                      8162 ccctgctgtgagctctggccgctgccttccagggctcccgagccacacgctggggggtgct 8221
                                                                    ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctcact 240
                                                                                              ttcagaagaagaagacagtaagcttgggtttttcagcagcggggggttctctctatttt 300
                                                                                                                                                                                                                                                                                                                                                                            Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia;
                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a human ABC1 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF24680 standard; DNA; 10442
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99US-0166573.
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                                                                                                                                   cagttaatgaccagccacgggggttcctgctgtcagctctggccgctgccttccagggct 156
                                                                                                                                                                                                                                                                     315 ttgctgctgtggaagaacctcactttcagaagaagaagacaacatgtcagctgttactggaa 374
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                                                                                                          Gaps
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                                                                             Score 159.4; DB 22; Length 10442;
Pred. No. 9.3e-39;
0; Mismatches 41; Indels 0;
                                       Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
                                                                                                                                                                                                                                                                                                                gcagcggggggttctctcttttttttttgtggttttgagttggg 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a human ABC1 polypeptide.
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/product= "ABC1 polypeptide"
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                                                                                                                                                                                                                                                                                                                                                                                             AAF24702 standard; DNA; 10442
                                                                               44.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..7076
                                                                                                       Matches 184; Conservative
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                                                                               Query Match
Best Local Similarity
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19-NOV-1999;
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The present sequence encodes a human adenosine triphosphate (ATP)
binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
membranes and utilises ATP hydrolysis to transport a wide variety of
substrates across the plasma membrane. ABC1 is a pivotal protein in
the apolipoprotein-mediated mobilisation of intracellular cholesterol
stores. ABC1 is defective in Tangier disease, a genetic disorder
characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
localised to chromosome 9422-9431. The ABC1 genes and proteins are
useful for developing pharmaceutical agents for the treatment of heart
clisease and other disorders associated with hypercholesterolemia and
atherosclerosis. The genes are useful for developing screening assays to
screen for compounds that regulate the expression of genes associated
with cholesterol transport. The genes and proteins are also useful for
are also useful as diagnostic indicators of cardiovascular disease and
cother disorders associated with hypercholesterolemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adenosine triphosphate binding cassette protein 1; ABC1; apoliopprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atheroscierosis; cholesterol transport; ss.
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                                                                                                                                                                                                                                                                                                                                     Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.6%; Score 159.4; DB 22; Length Best Local Similarity 81.8%; Pred. No. 9.3e-39; Matches 184; Conservative 0; Mismatches 41; Indels
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/product= "defective ABC1 polypeptide"
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99US-0166573.
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14-SEP-1999;
19-NOV-1999;
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) i polypepitde, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal Tangier disease, a genetic disorder characterised by corromosome 9922-9931. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
                                                                                                                  Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
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(CVTH-) CV THERAPEUTICS INC.
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20-APR-2001 (first entry)

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binding cassette protein (ABC) I polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises a Tangier disease patient. ABC1 resides in cell membranes and utilises. ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier diseases, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 942-9431. The ABC1 genes and proteins are useful for developing that required is for the treatment of heart disease and other classred with hypercholesterolesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol caracterolemic as alagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
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/product= "defective ABC1 polypeptide"
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                                                                                                                                                                                                                                                                                                                                       99US-0140264.
99US-0153872.
99US-0166573.
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14-SEP-1999;
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44.6%; Score 159.4; DB 22; Length 10474; 81.8%; Pred. No. 9.3e-39; tive 0; Mismatches 41; Indels 0; 0
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                                184; Conservative
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AAF24707 standard; DNA; 10474 BP

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                                                               Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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                                                                                                                               Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
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44.6%; Score 159.4; DB 22;
Best Local Similarity 81.8%; Pred. No. 9.3e-39;
Matches 184; Conservative 0; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garvin M;
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                                      Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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                                                                                                                                                 277 gcagcggggggttctctcttttttttgtggttttgagttggg 321
                                                                                                                                                                                                                      407 giggcetggcetetatitateticetgatectgatetetgtiegg 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          AAF24708 standard; DNA; 10474 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0140264.
99US-0153872.
99US-0166573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVTH-) CV THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB31367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1999;
19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents the partial coding sequence of human ABC1, which encodes amino acids 1-60 of the human ABC1 protein. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brewer HB;
                                                                                                            97 cagitaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggct 156
                                                                                 227 cagittaaigaccaggcacgggcgiccigcigigagcictggccgcigccitccagggci 286
                                                                                                                                                                   ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                                                                             347 ttgctgctgtggaagaacctcactttcagaagaagacaaacatgtcagctgttactggaa 406
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human ABC1 protein, amino acids 1 to 60"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol; cardiovascular; neurological; Tangier disease;, LCAT deficiency; lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
DB 22; Length 10474;
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Jaye M, Searfoss GH, Remaley A, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human ABC1 nucleic acids and polypeptides for treating
                            Indels
                                                                                                                                                                                                                          gcagcgggggttctctctatttttttgtggttttgagttggg 321
                                                                                                                                                                                                                                             44.6%; Score 159.4; DB 22;
81.8%; Pred. No. 9.3e-39;
Live 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 167; 368pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Partial human ABC1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                             AAS04035 standard; cDNA; 446 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosier-Montus M,
Duverger N, Jaye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2000; 2000WO-EP10886.
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                             Matches 184; Conservative
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                 Local Similarity
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Lemoine C,
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  Query Match
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tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttgctgctgttggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                                                                                                                                                                                                    209 ttgctgctgtggaagaacctcactttcagaagaagacaaacatgtcagctgctgctggaa 268
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                                                                                                                                                                                                                                                                                                                                                                           157 cccgagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgagg 216
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                 40.8%; Score 145.8; DB 22; Length 446;
80.9%; Pred. No. 3.7e-35;
iive 0; Mismatches 42; Indels 1;
                                                                                                                                                                                                                                                       42; Indels
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                                                                                                                                                          Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ABCAl homologue-encoding cDNA, SEQ ID NO:976.
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                     Best Local Similarity 80.9
Matches 182; Conservative
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P-PSDB; ABB11956.
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sequences ABA08225-ABA09574 represent incleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a furthed against the polypeptides, or producing the novel polypeptides, and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides or antibodies and asample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may of the polypeptides of the invention activities; is tem cell proliferation or cell have activities; reachior activity; issue growth activity; haematopolesis regulatory activity; tissue growth activity; haematopolesis regulatory activities; haemostatic, thrombotic or fundunomdulatory activity; activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be invention are useful for preventing, treating or ameliotating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions and unceres, namentopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions and unceres, namentopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions and conditions are useful prowth, polypeptides involved with tissue regeneration and repair growth, polypeptides involved with tissue regeneration and repair growth. Polypeptides involved with tissue regeneration and repair growth. Polypeptides involved with tissue regeneration and tental growth. Polypeptides involved with tissue tradement of viral, bacterial and fungal infections in addition to immune disease or accidental d
                                                                                                                                                                             Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                 treating or ameliorating a medical condition in a mammalian subject
                     Human proteins and DNA encoding sequences useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.8%; Score 145.8; DB 22; Length 7086;
80.9%; Pred. No. 1.3e-34;
Live 0; Mismatches 42; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
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                                                                       e.g. arthritis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.9
Matches 182; Conservative
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AAK52667 standard; cDNA; 7086 BP

RESULT 11 AAK52667

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                                                                                                                                                                                                                      cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ma Y;
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the sequence listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 cccgagccacacqctggggggggctgacggggaacatggcttgttggcctcagctgagg 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                    vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cccgagccacacgctgggcgtgctgagggaacatggcatgttggcctcagctgagg
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Zhang J, Ren F, Chen R, Wang 2W;
F, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Indels
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80.9%; Pred. No. 1.3e-34;
ive 0; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in diagnosis and gene therapy -
                                                                                                                          Human polynucleotide SEQ ID NO 2196.
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Wang D, Wang J, Zh
Yang Y, Wejhrman T,
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2000US-0598075.
2000US-0620325.
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2000US-0693325.
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                                           (first entry)
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Best Local Similarity 80.99
Matches 182; Conservative
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                                                                                                                                                                                                                      Human; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAM79534
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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20-JUN-2000;
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01-SEP-2000;
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20-OCT-2000;
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                                           06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
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Human, ATP binding cassette transporter 1; ABC1; coronary heart disease, dermatological; atheroscilenosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lobeta (IL-lobeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 cagttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggct 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                          388 gtggcctggcctctatttatcttcctgatcctgatctctgttcgg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                       277 gcagcggggggttctctcttttttttttgtggtttgagttggg
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80.9%; Pred. No. 1.3e-34;
ive 0; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                  AAD21326 standard; DNA; 7260
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Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      AAD21326;
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The present sequence is that of cDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AAM50227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAI70314, using an alternative ATG codon as initiation codon and thereby adding an
                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "alternative open reading frame of AAI70314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                           ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipaemic; antipsoriatic; dermatological; Tangier disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New adenosine triphosphate binding cassette transporter gene
                                                                                             277 geagegggggttetetetttttetttgtggttttgagttggg 321
                                                                                                            Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 26-28; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                 AAI70315 standard; cDNA; 7260 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(976, A)
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7106
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                                                                                                                                                                                                                                                                                                                               polymorphism; ss.
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
extra 40 N-terminal amino acids to the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the different Tangier Kindreds. In the variant genes (numbering as in different Tangier kindreds. In the variant genes (numbering as in AAT70314), G is changed to A at position 596. T is changed to C at position 1136. A is changed to G at position 2589 or G is changed to C at position 136. Or any combination of these. All of these polymorphisms alter the amino acid sequence of ABC1 and therefore polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2889G) are both associated with a decreased in vitro ApoA-1 mediated efflux of cholesterol from mononuclear phagocytes, a cature typical of Tangier disease. 3 of the variants (G596A, A289G and G3456C) are significantly increased in a population of men having low high density lipoprotein-cholesterol levels and established coronary heart disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular diseases, and inflammatory diseases (c.HD) relative cardiovascular erythematodes) is claimed. Modulation of ABC1 transcripts or proteins by antisense or ribozyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 ttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttca 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 cagttaatgaccagccacgggcgtcctgctgtcagctctggccgctgccttccagggct 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.8%; Score 145.8; DB 22; Length
80.9%; Pred. No. 1.3e-34;
Live 0; Mismatches 42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK51683 standard; cDNA; 7281 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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20-JUN-2000;
19-JUL-2000;
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                                                                                                                                  Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 cagttaatgaccagccacggcgtccctgctgtcagctctggccgctgccttccagggct 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 cccgagccacacgctgggggtgctggctgagggaacatggcttgttggcctcagctgagg 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol; cardiovascular; neurological; Tangier disease;, LCAT deficiency; lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                  Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 cccgagccacacgctggggggggggggggggaacatggcatgttggcctcagctgagg
                                                                                                                                               Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.8%; Score 145.8; DB 22; Length 7281; 80.9%; Pred. No. 1.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
                                                                                                                         Liu C, Drmanac RT, Asundi V, Zhou P, Xu C,
Wang D, Wang J, Zhang J, Ren F, Chen R, Wang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.3e-34;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                              Claim 1; Page 1086-1096; 6221pp; English.
                                                                                                                                                                                                                                                                 useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS06120 standard; cDNA; 9741 BP
                15-SEP-2000; 2000US-0663561
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
 01-SEP-2000; 2000US-0654936.
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Matches 182; Conservative
                                                                                                                                                                                             WPI; 2001-476283/51.
                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                 P-PSDB; AAM78550.
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                                                                                                                         Tang YT,
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The sequence represents the coding sequence #1 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing ardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                        Naudin L;
                                                                                                                                                                                                                                                                                                       Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L
Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 cagttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggct 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 ttgctgctgtggaagaacctcactttcagaagaagaacaacagtaagcttgggttttca 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 40.8%; Score 145.8; DB 22; Length 9741; Similarity 80.9%; Pred. No. 1.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                             New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
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                                                      /*tag= a
/product= "Human ABC1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 204-208; 368pp; English.
                  Location/Qualifiers
                                                                                                                                                                            26-OCT-2000; 2000WO-EP10886.
                                                                                                                                                                                                                               01-MAR-2000; 2000US-0186260.
                                                                                                                                                                                                                  99EP-0402668
                                                                                                                                                                                                                                                                   (AVET ) AVENTIS PHARMA SA.
                                   185..6967
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Matches 182; Conservative
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P-PSDB; AAU02176.
                                                                                                       WO200130848-A2.
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Lemoine C,
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Search completed: September 20, 2002, 03:08:57 Job time: 10606 sec

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September 20, 2002, 03:21:22; Search time 110.16 Seconds (without alignments) 796.035 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                383533 seqs, 122816752 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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357
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Issued\_Patents\_NA:\* Database

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/cgn2\_6/ptodata/2/ina/pcTUS\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/pcTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		Sequence 2, Appli	Ä	3,	'n	3,	3,	37,	25,	2, 2	7	7	7,	7,	'n	٦,	'n	'n	15,	'n	7,	7,	Sequence 7, Appli	Sequence 1, Appli	124,	Sequence 124, App	5, A	1,
	E		US-08-680-327-2	US-09-228-246-1	US-08-462-195-3	US-08-636-883-3	US-09-127-829-3	US-09-173-914-3		US-08-397-220B-25	US-08-866-650-2	US-09-021-287-2	US-09-240-473-2	US-08-574-043A-7	US-08-795-015-7	US-08-751-189-1	US-09-060-836-1	US-09-184-445-1	US-09-144-085-3	US-08-609-657-15	US-09-534-638-3	US-08-781-802-7	US-08-694-078-7	US-09-058-260-7	US-09-360-186-1		PCT-US95-10398-124		US-08-083-590A-1
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	arcos.		31	31	30.8	30.8	30.8	30.4	30	30	30	30	30	30	30	30	30	30	30	29.6	29.4	29.4	29.4	29.4	29.4	29.5	29.5	29.5	29.5
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Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Seguence 1, Appli	Sequence 5, Appli	Seguence 1, Appli	Sequence 1, Appli	Sequence 10, Appl	Seguence 7, Appli	Seguence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Seguence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 115, App
US-08-465-500-5	US-08-346-126-5	US-08-346-128-5	US-08-532-384-1	US-08-893-828-5	US-08-640-906-1	US-09-395-936-1	US-08-482-073-10	US-07-914-281-7	US-08-393-246-7	US-08-525-058A-7	US-08-696-731-7	US-09-042-531-7	US-08-324-977-7	US-08-384-616-7	US-08-904-686A-7	US-09-315-850-7	US-08-290-665A-115
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2892	2892	2892	2892	2892	1257	1257	2861	3647	3647	3647	3647	3647	345	345	345	345	573
8.2	8.5	8.2	8.3	8.2	8.1	8.1	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0
29.3	29.5	29.5	29.5	29.3	28.8	28.8	28.6	28.6	28.6	28.6	28.6	28.6	28.4	28.4	28.4	28.4	28.4
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## ALIGNMENTS

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APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edward, APPLICANT: Staskawicz, Dohn M., Rommens, Caius TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT TITLE OF INVENTION: PATHOGEN RESISTANCE NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
COMPUTER: BW PC compatible
OPERATING SYSTEM: MS DGS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/680,327
FILING DATE: July 11, 1996
CLASSIFICATION BORN:
APPLICATION NAME: 800
PRIOR APPLICATION NAME: 08/310,912
FILING DATE: September 22, 1994
CLASSIFICATION: 800
APPLICATION NUMBER: 08/227,360
FILING DATE: APPTIL 13, 1994
CLASSIFICATION NUMBER: 08/227,360
FILING DATE: APPTIL 13, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 5151-45038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10968 base pairs
                                                                                                                                                                                                                                                                                                                 STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
STREET: Portland
STATE: Oregon
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double stranded
                   Sequence 2, Application US/08680327
Patent No. 5859321
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-680-327-2
US-08-680-327-2
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CORRESPONDENCE ADDRESS
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US-08-636-883-3/C
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                                                                                                                                           Compositions
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                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences:
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
FILE REFERENCE: 51700
CURRENT APPLICATION NUMBER: US/09/228,246
CURRENT FILING DATE: 1999-01-18
EARLIER APPLICATION NUMBER: 08/680,327
EARLIER PILING DATE: 1994-09-22
EARLIER FILING DATE: 1994-09-22
EARLIER PILING DATE: 1994-04-13
EARLIER FILING DATE: 1994-04-13
SAFAIRE FILING DATE: 1994-04-13
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                269 gitticagcagcgggggttctctctatttttctttgggtttggagttg 319
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                                     DB 2; Length 10968;
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55.0%; Pred. No. 6.2;
tive 0; Mismatches 50; Indels
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APPLICANT: SATTO, IZUMU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: SEKI, MAKOTO
TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 9
                                                                              50; Indels
                                  Score 31; DB 2
Pred. No. 6.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09228246
Patent No. 6245510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Lycopersicon esculentum
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Patent No. 5789544
GENERAL INFORMATION:
                                  Query Match 8.7%;
Best Local Similarity 55.0%;
Matches 61; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.0%
....rhes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (8300)..(9466)
US-09-228-246-1
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LOCATION: (3879)..(8186)
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107 ccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctcccgagccac 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1037;
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30.8; DB 1; Length 1 Pred. No. 2.1; 0; Mismatches 117; Indels
      ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,303
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5789544man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,195
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 413-3000
TELEFRAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
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Similarity 46.3%;
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LENGTH: 1037 base pairs
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EDNESS: double
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                                                                                           i: Virginia
PRY: U.S.A.
22202
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STRANDEDNESS:
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                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                COUNTRY:
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Matches 101;
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227 ggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcggggg 286
                                                                            117 ACTCCACCAACGATCTGACCACCGCCCGGGAACTTAACGTCCTGTGGGCGGCGGTTGGTG 58
                                                                                                                                                287 gttctctcatttttctttgtggttttgagttggggat 324
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,303
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09127829
Patent No. 6063904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MIYAMURA, TATSUO
APPLICANT: SATTO, IZUMU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
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TYPE: nucleic acid
STRANDEDNESS: double
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17..1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-09-127-829-3
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US-09-127-829-3/c
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46.3%; Pred. No. 2.1;
tive 0; Mismatches 117; Indels 0.
                                                                                               APPLICANT: MITAMATAN.
APPLICANT: MITAMATAN.
APPLICANT: MATSUDA
APPLICANT: MATSUDA
APPLICANT: MATSUDA
APPLICANT: MATSUDA
APPLICANT: HONDA, YOSHIMARU
APPLICANT: BEKI, MAKOTO
TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF
TITLE OF INTENTION: MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: ALINGTON
STREE: VITGING ON STATE: VITGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/636,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-UN-1993
APPLICATION NUMBER: UP 152487/1992
FILING DATE: 11-UN-1992
ATTORNEY AGENT INFORMATION:
NAME: ODION, NO. 5830691man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4169-003-0
TELECOMMUNICATION INFORMATION:
FELEPHONE: (703) 413-3000
TELECAK: (703) 413-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 3, Application US/08636883
Patent No. 5830691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Hepatitis C virus
IMMEDIATE SOURCE:
CLONE: PUCM010
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E: DNA (genomic)
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Best Local Similarity 46.39
Matches 101; Conservative
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; LOCATION: 17..1036
US-08-636-883-3
                                                                            GENERAL INFORMATION:
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,829
57 TTACGTTTGATTTTTCTTTGGGGTTTTGGATTTGTGCT 20
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APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: JP 152487/1992
FILING DATE: 11-JUN-1992
ATTONNEY/AGENT INFORMATION:
NAME: Oblon, No. 6063904man F.
REFIERNCE/OOCKET NUMBER: 4169-003-0
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION OF SECONDAL O
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GENERAL INFORMATION:

APPLICANT: Hendrickson, Eric

APPLICANT: Hendrickson, Eric

TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: Methods of Regulating DNA Dependent Frotein Kinase Activity

TITLE OF INVENTION: Webbase of Regulating DNA Dependent Frotein Kinase Activity

CURRENT APPLICATION NUMBER: US/09/173,914

CURRENT FILING DATE: 1998-10-16

EARLIER APPLICATION NUMBER: 60/064,557

BARLIER FILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                     167 acgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctgctgt 226
                                                                                                                                                                                                                                  177 TCGGAAGTCTTCCTAGTCGCGCGCACACCCAACCTGGGGCCCCTGCGGGCAACAGGTAA 118
                                                                                                                                                                                                                                                                                       227 ggaagaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcggggg 286
                                                                                                                             237 CTACCCTCGGGTTGGCGAGCCTTGGGGATAGGTTGTCGCCTTCCACGAGGTTGCGGCCGC 178
                                                                                                                                                                                                                                                                                                                                       117 ACTCCACCAACGATCTGACCACCGCCCGGGAACTTAACGTCCTGTGGGCGGCGGTTGGTG 58
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  46.3%; Pred. No. 2.1;
tive 0; Mismatches 117; Indels
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
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STREET: 66 East Main Street
CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                            57 TTACGTTTGATTTTTCTTTGGGGTTTTGGATTTGTGCT 20
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8.5%; Score 30.4; DE
Best Local Similarity 57.3%; Pred. No. 4.5;
Matches 55; Conservative 0; Mismatches
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APPLICANT: Kevin P. Anderson et al.
TITLE OF INVENTION: Compositions Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/08988321B Patent No. 6174868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09173914 Patent No. 6171857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mesocricetus Auratus US-09-173-914-3
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                             Matches 101; Conservative
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CORRESPONDENCE ADDRESS:
Best Local Similarity
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STATE:
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46.3%; Pred. No. 3.1;
tive 0; Mismatches 115;
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ADDRESSE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 tctcatttttttttgtggttttgagttggggat 324
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OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFRENCE/DOCKET NUMBER: 1SPH-0245
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
INFORMATION FOR SEO 1D NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                     US/08/988,321B
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: September 10, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 25, Application US/08397220B
; Patent No. 6284458
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/945,289
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,093
FILING DATE: May 17, 1996
                                                                                                                                                                                                                                       08/452,841
                                                                                             FILING DATE: December 10, 1997
                                                                                                                                                                                                                                                              FILING DATE: May 30, 1995 PRIOR APPLICATION DATA:
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                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: Single
                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear ANTI-SENSE: NO
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Best Local Similarity
Matches 99; Conserv
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                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-397-220B-25/c
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Pred. No. 3.1;
0; Mismatches 115; Indels
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Tekahara, Kuzuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
WUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/01293
FILING DATE: 10.5ep-93
APPLICATION NUMBER: JP 5-87195
FILING DATE: 14-Apr-93
APPLICATION NUMBER: 07/945,289
FILING DATE: 10.5ep-92
ATTONEY/AGENT INFORMATION:
NAME: Jane MASSEW Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-8488
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 GITTGGITTTTCTTTGAGGTTTAGGATTCGTGCT 345
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                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/397,220B
FILING DATE: 09-Mar-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-397-220B-25
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STREET: 1 South Pinckney Street
                                                                    SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08866650 Patent No. 5939321 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.3%;
Matches 99; Conservative
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
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0; Gaps
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8.4%; Score 30; DB 2; Length 4771;
Best Local Similarity 52.4%; Pred. No. 8.5;
Matches 66; Conservative 0; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,287
        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                             960296.93839
                                                                         us/08/866,650
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ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/866,650
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Patent No. 5981717
                                                                                         FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REPERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
IBM PC compatible
                                                                                                                                                                                                                                 TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 4771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
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LOCATION: 611..3652
                                                                         APPLICATION NUMBER:
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CITY: Madison
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8.4%; Score 30; DB 2; Length 4771;
Best Local Similarity 52.4%; Pred. No. 8.5;
Matches 66; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 611..3652
OTHER INFORMATION: /product= "murine mīll protein"
US-09-031-287.1
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Patent No. 6297011
GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/240,473
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPAN: 608-251-5000
INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 4771 base pairs
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STREET: 1 South Pinckney Street
CITY: Madison
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TELECOMMUNICATION:
TELEPHONE: 608-251-5000
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NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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COUNTRY:
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                                                                                                                                                                                                                                                                     8.4%; Score 30; DB 4; Length 4771; 52.4%; Pred. No. 8.5; tive 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                            60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kinzler, Kenneth W.
APPLICANT: El-Deiry, Wafik
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: p21WAF1 Derivatives and Diagnostic
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                               COTATION: 611..3652
COTHER INFORMATION: /product= "murine mTll protein"
US-09-240-473-2
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REGISTRATION NUMBER: 32,141
REFERNCE/DOCKET NUMBER: 01107.49698
TELECOMMINICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 7:
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MEDIUM TYPE: Floppy disk
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                       LENGIH: 4771 base pairs
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LENGTH: 5143 base pairs
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SEQUENCE CHARACTERISTICS:
                                      nucleic acid
EDNESS: double
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STRANDEDNESS: double
                                                                                                                                            NAME/KEY: CDS
LOCATION: 611..3652
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                         TYPE: nucleic STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kinzler, Kenneth W.
APPLICANT: E1-Deiry, Wafik
APPLICANT: Vogelstein, Bert
IITLE OF INVENTION: p21WAF1 Derivatives and Diagnostic
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,015
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ER: 01107.49698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/574,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08795015 Patent No. 5871968 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kagan, Sarah A.
REGISTRATTON UNUBER: 32,141
RELECOMMUNICATION INFORMATION:
TELEPRONE: 202.508.9100
TELEPAX: 202.508.929
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  4300 GCCACAAATCTGGCTTTTTTA 4279
                                                                                                                                                                                                                                                                                                                                                                            255 aacagtaagcttgggtttttca 276
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MOLECULE TYPE: DNA (genomic)
                                             POSITION IN GENOME:
CHROMOSOME/SEGMENT: 6p21.2
US-08-574-043A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Homo sapiens
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                     CELL LINE:
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                                                                                                                                                                                                                                                  195 ggcatgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagaca 254
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Patent No. 5919656
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5919656el Genes Encoding Telomerase Protein TITLE OF INVENTION: 1.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                   8.4%; Score 30; DB 2; Length 5143; 50.7%; Pred. No. 8.8; tive 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                   4300 GCCACAAATCTGGCTTTTTTA 4279
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ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Namey A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 1:
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CELL LINE: GM
POSTITION IN GENOME:
CHROMOSOME/SEGMENT: 6P21.2
US-08-795-015-7
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 48.8'
Matches 81; Conservative
                                                                                                                               Query Match 8.4%
Best Local Similarity 50.7%
Matches 72; Conservative
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; MOLECULE TYPE: CDNA
US-08-751-189-1
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ZIP: 91320-1789
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5166 IGCTIGITIGITCCTCTCCGAIGAIACACTCTTTCTIACIGCCTTCGACGGGCTCCTGGA 5225
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APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 tgatggctgtttcccctcctgctttatctttcagttaatgaccagccacgggcgtccctg 125
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48.8%; Pred. No. 11;
tive 0; Mismatches 85; Indels
                                                                5226 GCTCTGGGACCTGCAGCATGTTGGGGGTGCTGCAGAGCT 5271
                                         126 etgteagetetggeegetgeetteeagggeteeegageeacaeget 171
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STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZUTE: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/060,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 20, 2002, 03:21:31
Job time: 14180 sec
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTATION NUMBER: 34,688
REGISTATION NUMBER: 34,688
                                                                                                                                                                  US-09-060-836-1
; Sequence 1, Application US/09060836
; Patent No. 5981707
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LENGTH: 7881 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 48.8%
Matches 81, Conservative
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; MOLECULE TYPE: CDNA
US-09-060-836-1
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September 20, 2002, 01:23:10 ; Search time 3895 Seconds (without alignments) 1237.076 Million cell updates/sec
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357
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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EST:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

12	12 BHU8/81/ BHU8/81/	10 BG305753 BG30575	9 BB841907 BB84190	12 A0848626 AQ8486	12 CNS006ST AL0658	10 BF128237 BF1282	10 BE733920 BE7335	12 CNS0162E AL1062	9 AW751638 AW75163	9 BB843149 BB84314	10 BF484412 BF4844	10 BE471178 BE4711	10 BE/48387 BE/483	12 CNSOUETV ALUGUE	12 CNS03ZIU ALZ6/C	12 CNSU06UU ALU65S	TO CNSOTOFIO PROPERTY ALONG OF STREET	12 CNSOOE1V ALO787	9 AU212427 AU212427	10 BI886434 BI8864	9 AW681359 AW681359 I	12 CNS00BP8 AL057462	12 CNS010C9 AL098787	1201 12 CNS01604 AL106126 Drosophil 468 12 AQ773862 HS_2254_A	ALIGNMENTS		C TOG recail ANDM ad	/36 DP MKNA LINEAR 24 CCI-2000 PLACE1 Homo sapiens cDNA clone PLACE1002437 5', MRNA		GI:10996127			Chordata: Craniata: Vertebrata;	Eutheria; Primates; Catarrhini; Hominidae; Homo.	, Suzuki,Y., Ishii,S., Saito,K., Kawa	a, Y., Nagai, T.,	cDNA project	d (2000)	akao isogai aboratory	0.00	a, nisarazu, Chiba 292-0812, Japan 8-52-3951	Fax: 81-438-52-3952	3'-end one nass segmenting:	s end one pass seque ry construction: Depa	Science, University of Toky	earch Institute. Location/Qualifiers	1736 /organism="Homo sanions"	db_xref="taxon:9606"	clone="PLACE1002437"	cione_iib= runchi tissue_type="placenta"	note="Vector: pME18SFL3"
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Query Match
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagama, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB657864 RIKEN full-length enriched, 12 days embryo eyeball Mus musculus cDNA clone D230019D04 5', mRNA sequence.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1517-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                        97 cagttaatgaccagccacggggggtcctgctgtcagctctggccgctgccttccagggct 156
                                                                                                                                                                                                             157 cccgagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgagg 216
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                                                         Gaps
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                                                      Indels
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
     DB 9;
  Score 144.2; DB 9
Pred. No. 8.3e-28;
                                                    0; Mismatches
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Query Match
Best Local Similarity 80.4%;
Matches 181; Conservative
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COMMENT
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485128081 normalized infant brain cDNA Homo sapiens cDNA clone c-12508, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 185 c 173 g 134 t l others
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, 12 days embryo eyeball"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 cagttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggct 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 cccgagccaca-----cgctgggcgtgctggctgagggaacatggcatgttggcct 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 CTCGAGCCGCAGACGCAGGTCGCTGTGGGTGCCGGCTGTGGTGACATGGCTTGTTGGCCT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 cagitaargaccagccac-agagicacagcrererecreregerecrecoreceageer 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.2%; Score 75.8; DB 9; 77.8%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                              /dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="D230019D04"
                                                                                                                                                                                                                                                                                                                                       /tissue_type="eyeball"
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z44377.1 GI:573506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 133; Conservative
                                                                                                                     e mouse tissues.
                                                                                                                                                                      .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
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/tissue_type="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
siolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
50 a 87 c 96 g 56 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 535)
2 Eahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                  Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1zb08
Seq primer: (-21)M13_universal.
Location/Qualifiers
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%; Score 73.8; DB 10; Length 292; llarity 94.5%; Pred. No. 3.4e-09; Conservative 0; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 bp mRNA linear
303216 MARC 1PIG Sus scrofa CDNA 5', mRNA sequence.
BG384217
                                                                                                                                                                                                                                                                                                                                                          /clone_lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 cccgagccacacgctgggcgtgctggctgag 187
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-12b08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 CCCGAGCCACACGCTGGGGGTGCTGGCTGAG 292
                                                                                                                                     Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACKWARD: GITITCCCAGICACGACG
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                                                                                                              Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                Single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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KEYWORDS
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                                                                                                                                                                                                                                       FEATURES
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished 2 (base 1 to 982)

Coases 1 to 982)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Barnin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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1 (bases 1 to 982)

10 (bases 1 to 982)

11 (bases 1 to 982)

12 (bases 1 to 982)

13 (bases 1 to 982)

14 (bases 1 to 982)

15 (bases 1 to 982)

16 (bases 1 to 982)

17 (bases 1 to 982)

18 (bases 1 to 982)

18 (bases 1 to 982)

19 (bases 1 to 982)

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11 (bases 1 to 982)

12 (bases 1 to 982)

13 (bases 1 to 982)

14 (bases 1 to 982)

15 (bases 1 to 982)

16 (bases 1 to 982)

17 (bases 1 to 982)

18 (bases 1 to 982)

19 (bases 1 to 982)

10 
                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 cagittaaigaccagccacggggggtcccigctgtcagcictggccgctgccttccagggct 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 CAGITAAIGACCAGGCCACAG -- CGCCCCIGCIIGAGCICIGGCCACTICCICCACGGGGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 TCCCGAGCGGAGCCACACGCAGGCTGGTGTGGTGCCAGCTGAGGTAACATGGCTTATTGG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Gaps
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                                                                                                                                                               /organism="Sus scrofa"
                                                                                                                                                                                                            /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
Plate: 90 row: G column: 13
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
                                                                                      Location/Qualifiers
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AUTHORS
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/organism="Tetraodon nigroviridis"

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Useroscope.

Direct Submission

Lead (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Manmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI disestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's pland And how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://www.ifile.
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                                                                                                                                                                                                                                                                                                    237 cactitcagaagaagacaaacagtaagcitgggittitcagcagcgggggggttctctcat 296
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                                              /clone_lib="G" //clone_lib="G" //note="Genoscope sequence ID : C0AG260CH10SP1~end :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 910)
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                                                                                                                                                                                                               Length 982;
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                                                                                                                  17 others
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                                                                                                                                                                                                          11.9%; Score 42.4; DB 12;
55.0%; Pred. No. 0.86;
ive 8; Mismatches 46;
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/db_xref="taxon:99883"
/clone="260P19"
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Drosophila melanogaster
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Enkaryota; Entamoebidae; Entamoeba.

Eukaryota; Entamoebidae; Entamoeba.

Elvaryota; Entamoebidae; Entamoeba.

Enfus, B., Van Aken, S. and Fraser, C.

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HMI:MSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bloftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

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/strain="HM1: MSS"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared Forestructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kD). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Waking small insert Inbraries for
                                                                                                                                                                                                                                                                                                                                                                                AZS42175 926 bp DNA linear GSS 14-NOV-2000 ENTGP86TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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289 tototoattttttttttgtggttttgagttggggattggaggagggagggagggaaggaa
                                                                                                                 228 gaagaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcgggggg 287
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Pred. No. 18;
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High quality sequence start: 17
High quality sequence stop: 297.
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A2542175
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Best Local Similarity 57.1%;
Matches 68; Conservative
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Mismatches

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64;

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Similarity

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229 aagaacctcactttcagaagaagacaaacagtaagcttgggtttttcagcagcggggggt 288

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us-09-846-456-2.std.rst

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Email: satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ciona intestinalis"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                        Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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113 c 94
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                                                                                                                                                                AV845237.1 GI:16823451
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Department of Zoology
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Local Similarity 51.5%;
les 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                           440 bp mRNA linear EST 14-APR-1998 vz01f08.r1 Soares_mammary_gland_NDAMG Mus musculus cDNA clone IMAGE:1314471 5', mRNA sequence.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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181 ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctc 237
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Contact: Marra MyMouse EST Project
Contact: Marnum WnWouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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AV864011 AVI Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone rcieg37m02 3', mRNA sequence.
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1 (basea: 1 to 571)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
   EST 08-NOV-2001
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 533)
Satoh, N., Satou, Y., Kohara, Y. and Shin-1, T.
Expressed genes in Ciona intestinalis
Unpublished (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="rcieg08618"
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AV845237 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone rcieg08c18 3', mRNA sequence.
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EST 29-APR-1999

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1to 322)
Yamamoto,K. and Sasaki,T.
Yamamoto,K. and Sasaki,T.
Rice CoNA from mature leaf
Unpublished (1999)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tsassaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                 322 bp mRNA linear EST 29-APR AU056364 Oryza sativa mature leaf Nipponbare Oryza sativa cDNA AU056364
           98 agttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctc 157
                                                  198 AGAATATGGAGAGCCAAAGATCTGCATGTTCTGTACACTGAACTCTGCTTTTATTGGATC 139
                                                                                          158 ccgagccacacgctggcgtgctgactgagggaacatggcatgttggcctcagctgaggt 217
                                                                                                                                    138 AAAATGCCAACGCTGTGCCAGCAGTAAGAAGAAATATGGAATGCCAGTCAATTGTCAGAA 79
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100 c 103 g 82 t
                                                                                                                                                                     218 tgctgctgtggaagaacctcactttcagaagaagacaaacagtaag 263
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/organism="Oryza sativa"
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
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Best Local Similarity 53.0%
....has 75, Conservative
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Oryza sativa
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AU162694
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AU056364
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AV892280 Nori Satch unpublished cDNA library, young adult Ciona intestinalis cDNA clone rclad32b06 3', mRNA sequence.
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Ciona intestinalis.
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
I (basea: I to 579)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
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Pred. No. 31;
0; Mismatches 81; Indels (
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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/dev_stage="young adult"
il6 c 102 g 203 t
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117 c 98
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Best Local Similarity 51.2%;
Matches 85; Conservative
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AU162694 AU162694 Rice mature leaf Oryza sativa cDNA clone S20642, mRNA
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                                                                                                                 213 gaggttgctgctgtggaagaacctcactttcagaagaagacaaacagtaagcttgggttt 272
                                                                                                                                                                   273 ttcagcagcggggggttctctctattttttttgggttttgagttggggattggaggag 332
                                                                                                                                                                                                                                                          243 GTTTGGTGCTGGGGGTTGGGTTGGTTGGTTGGTTTGGAGATGTTTCGGGAG 302
                                                             0; Gaps
10.1%; Score 36; DB 9; Length 322; 53.6%; Pred. No. 37; tive 0; Mismatches 65; Indels
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 872)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Second Collius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Benost, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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1 (basea: 1 to 571, Kohara,Y. and Shin-i,T.

Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
                                                                                    Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeee; Oryze.

Ehrhartoideae; Oryzeee; Oryze.

Sasaki, T. and Yamamoto, K.

Sasaki, T. and Yamamoto, K.

Unpulished (2000)

Contact: Takuji Sasaki

National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                       Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                    Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AX060894 AF287263 AC103155 AP000302 AP000046

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Homo sapi Sequence Sequence

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BC016252 LMFLCHR31\_18

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PAT 06-FEB-2002
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 4 08-NOV-2001;
Aventis Pharma S.A. (FR)
                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 62 c 73 g 42
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Sequence 4 from Patent W00183746.
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Homo sapiens ATP binding cassette transporter 1 (ABCA1) mRNA,
partial cds.
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/protein_id="AAF69513.1"
/protein_id="AAF69513.1"
/db_xref="G1:7769708"
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University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
Location/Quallifiers
1, 697
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Analysis of hAEL, gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 697)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fileding, C.J. and Kane, J.P..
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Pred. No. 5.4e-49;
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ilarity 100.0%; Pred. No. 5.4
Conservative 0; Mismatches
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1. .>697
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Length 697;

Score 221; DB 9; Pred. No. 5.7e-49;

100.0%; 100.0%;

Query Match Best Local Similarity

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1167)

Porsch-Ozcurumez,M., Langmann,T., Heimerl,S., Borsukova,H., Kaminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G. The zinc finger protein 202 (znf202) is a transcriptional repressor of atp binding cassette transporter al (abcal) and abcgl gene expression and a modulator of cellular lipid efflux J. Blol. Chem. 276 (15), 12427-12433 (2001)
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Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for
Clinical Chemistry, Universitiy of Regensburg,
FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
                                                                             ccgggctgcggcagggcagggcgggagctccgcgcaccaacagagccggttctcagggc 120
                                                                                               121 gctttgctccttgttttttccccggttctgttttctccccttctccggaaggcttgtcaa 180
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/function="cholesterol efflux regulatory protein"
315 c 327 g 247 t
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ABC-1 gene; ATP-binding cassette transporter-1; promoter.
human.
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Homo sapiens partial ABC-1 gene for ATP-binding cassette
transporter-1, 5'UTR and promoter region.
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/chromosome="9"
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Porsch-Oezcueruemez, M.K.
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Location/Qualifiers
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Schmitz, G. and Bodzioch, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-APR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1167)

Pullinger C.R., Hakamata H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Analysis of hABCI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

Blochem. Blophys. Res. Commun. 271 (2000) In press
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
                  ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
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promoter and exon 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence update by submitter
On Jun 23, 2000 this sequence version replaced gi:7769713
Location/Qualifiers
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Willinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aoulzert, B.E., Fielding, C.J. and Kane, J.P.
Direct Submission
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/db_xref="taxon:9606"
/chromosome="9"
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224. 844
/gene="ABCA1"
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NOV-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 6.3e-49;
tive 0; Mismatches 0;
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AX253452
AX253452.1 GI:16073979
                                                                                                                        3231 bp
Sequence 1 from Patent WO0183746.
AX351029
AX351029.1 GI:18616385
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/db_xref="taxon:9606"
1 773 c 876 q 773
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of Pieter de Jong. For further details see

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Liect submission

Submitted (11-JAN-2022) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 15, 2002 this sequence version replaced gi:18121468.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; WP; WORMPEP; Information on the WORMPEP that were allowed the supplementation on the WORMPEP.
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Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 6.6e-49;
ive 0; Mismatches 0;
                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
1765 c 1905 g 1756 t
Patent: WO 0170810-A 3 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
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AL359182.20 GI:18151453
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Matches 221; Conservative
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Direct Submission
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Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-21787 is from the library RPCI-11.1 constructed by the group

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sections only once, except for a short overlap.
The true right end of clone RP11-217B7 is at 96717 in this sequence. The true left end of clone RP11-122F10 is at 72980 in this sequence. The true right end of clone RP11-31320 is at 2000 in this sequence.
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Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Peneng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92050. .92163
//note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                              {\tt IMPORTANT:} This sequence is not the entire insert of clone {\tt RPI1-217B7} It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Sequence from AF275948 sequenced by National
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/note="Sequence from overlapping clone RP11-122F10
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HOMO Sapiens ABCAl (ABCAl) gene, complete cds.
AF275948
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http://www.chori.org/bacpac/home.htm
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/db_xref="taxon:9606"
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3238. .3278
                                                                                                                                                                                                                                  Location/Qualifiers
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92050. .92
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                VECTOR: pBACe3.6
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Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000) 20345099
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A., Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E., Francois,T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                      Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
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Eliren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collangelo, M., Collins, S., Collymore, A., Cooke, P., Darellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardf, G., Hagos, B., Headford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McGunghlin, J., Meldrim, J., Merrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. (Shome) Control of this sequence version replaced gi:6454033.

All repeats were identified using RepeatMasker:

Smit, A. F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 17504)
Birren, B., Linfon, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-1M10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13: M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 117571 bases at least Q40 Consensus quality: 117571 bases at least Q30 Consensus quality: 160940 bases at least Q30 Insert size: 185000; agarose-fp Insert size: 171264; sum-of-contigs Quality coverage: 2.9 in Q20 bases; sum-of-contigs Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L2510
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17200: contig of 1872 bp in length
30: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1003: contig of 1003 bp in length
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2735 4415: cont
4416 4515: gap of
4516 5785: cont
5786 5885: gap of
5886 7879: cont
7880 7979: gap of
7880 7979: gap of
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1104 2634: cor
                                                                                             Unpublished 2 (bases 1 to 175064)
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1454 GTAATTGCGAGCGAGAGTGAGTGAGTGGCCCGGACCCCCCGCAGAGCCGACCCTTCTCTC 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1514 CCGGGCTGCGGCAGGCAGGCGGGGAGCTCCCGCGCACAACAGAGCCGGTTCTCAGGGC 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 221; DB 9;
Pred. No. 7.9e-49;
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103117 103116; gap of 100 bp 103117 103116; gap of 100 bp 109178 contig of 6062 bp in length 109179 109278; gap of 100 bp 117308 117407; gap of 100 bp 117408 124079; gap of 100 bp 117408 124079; gap of 100 bp 131282 131381; gap of 100 bp 131382 138059; contig of 6678 bp in length 13182 131815; gap of 100 bp 1318159; gap of 1
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48116: contig of 2568 bp in length

48216: gap of 100 bp

52618: contig of 4402 bp in length

52718: gap of 100 bp

56592: contig of 3874 bp in length
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97901: contig of 4302 bp in length
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25707: contig of 3020 bp in length
07; gap of 100 bp
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2735. .4415
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AF2001 Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1) and SNAP protein genes, complete cds.
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Best Local Similarity 100.0%; Pred. No. 8e-49;
Matches 221; Conservative 0; Mismatches 0; Indels 0;
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59736. .63661
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7980. .9686
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SOURCE

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/translation="MACWPQLRLLLWKNLTFRRQTCQLLLEVAWPLFTFLILISVRL
SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIV
ARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clases 1 to 201144)
Qiu,Y., Caveller,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="AAK43526.1"
                                                                                                                                                                                                                                                                                        Qiu,Y., Cavelier,I., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse abcal comparative sequencing and transgenesis studies revealing novel regulatory sequences Genomics 73 (1), 66-76 (2001)
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78931. 79049,101048. 101169,104152. 104328,11728

123329. 122569,125285. 12544,125754. 125870,

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99.5%;
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HOMO sapiens clone RPl1-1N10, LOW-PASS SEQUENCE SAMPLING.
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1 (bases 1 to 69570)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-1N10
Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 183999)

1 (bases 1 to 183999)

1 (bases 1 to 183999)

Compositions and methods for modulating hdl cholesterol and triglyceride levels

Patent: Wo 0115676-A 1 08-MAR-2001;

University of British Columbia (CA); Xenon Genetics Inc. (CA)

Location/Qualifiers
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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tircil, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission
                                                                                                       Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced g1:6705871. All repeats were lidentified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                            sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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f 841 bp in length
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f 800 bp in length
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of 844 bp in length
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f 869 bp in length
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10376: contig of 846 bp in length
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14342 15196: contig of 855 bp in length
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17173 18041: contig of 869 bp in length
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19966: contig of 857 bp in length
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contig of 849 bp in length
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2905 3745: contig of
3746 3845: gap of 10
3846 4696: contig of
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7610 8479: contig of
8480 8579: gap of 10
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12303 12402: gap of
13280: cont
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16224 17072: cont
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7509: c
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11 31510: gap of 100 bp 13368: contig of 858 bp in length 133468: contig of 848 bp in length 133412: gap of 100 bp 100 bp 13342: gap of 100 bp in length 13 34268: contig of 856 bp in length 159 3458: contig of 836 bp in length 150 35204: contig of 836 bp in length 150 35204: contig of 836 bp in length
                                                                                                                                                100 bp
f 853 bp in length
100 bp
f 837 bp in length
                                                                                                                                                                                                                      100 bp
f 851 bp in length
100 bp
f 855 bp in length
66: gap of 100 bp
2021: contig of 855 bp in length
21: gap of 100 bp
21865: contig of 844 bp in length
                                                                        65: gap of 100 bp length
22832: contig of 867 bp in length
32: gap of 100 bp
23780: contig of 848 bp in length
                                                                                                                                                                                                                                                                                                                                                                           12: gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 1110 contig of 855 bp in length
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42824: contig of 811 bp in length
42924: gap of 100 bp
43776: contig of 852 bp in length
43876: gap of 100 bp
44752: contig of 876 bp in length
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48551: contig of 852 bp in length
651: gap of 100 bp
49485: contig of 834 bp in length
585: gap of 100 bp
50440: contig of 855 bp in length
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840 bp in length
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28532: contig of 856 bp in length
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contig of 856 bp in length
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33: contig of
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52372: contig of
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41913: cont
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27576: con
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31410: con
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LLSICAACNPKVEFHEHHILEHFSFCVCVSVSLFPAKGIVSFSWASFRIWVLWKAVFWQ
HGESKAVWEGQLGGHNILEFFSILVG"
363 C 399 9 414 t
               Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@Hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) MEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'-63'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Centerect), and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 29-SEP-2000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogal, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J.,
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oligo capping; fis (full insert sequence).
Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMA1
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AK022254
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/tissue_type="placenta"
/clone_lib="ptACE1"
/note="cloning vector: pME18SFL3"
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0; Mismatches 1
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2 (bases 1 to 1556)
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Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1002437.
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66684; contig of 844 bp in length
66784; gap of 100 bp
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                                                                                                                                                                                                                                                                   NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' = 8'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                            Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 90698)

Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.
NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 tttgetcettgttttttccccggttctgttttctccccttctccggaaggcttgtcaagg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TITGCICCTIGITITICCCCGGTICTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999ct9c9gcagggcagggcggggagctccgcgcaccaacagagccggttctcagggcgc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGGCTGCGGCAGGCGCGGGGGGGGGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccgacctttttctccc 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU21345 90698 bp DNA linear HTG :
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING
AC021345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-24J9
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Mammary gland"
/note="cloning vector: pME18SFL3"
489 c 586 g 384 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 219; DB 9; L
100.0%; Pred. No. 2.1e-48;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GGTAGGAGAAAGAGGCGAAACACAAAAGTGGAAAACAG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAMMA1000851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="MAMMA1"
                                                                                                         Isogai, T. and Otsuki, T. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC021345.2 GI:9130845
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                                                      Unpublished (2000) 2 (bases 1 to 1750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC021345/c
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                                                                                                                                      TITLE
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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKenan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisan, I.C., Pollara, V., Raymond, C., Rilegy, R., Rothman, D., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced g1:6705761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 10857; gap of 100 bp 11732; contig of 875 bp in length 13132; gap of 100 bp 100 bp 11732; contig of 907 bp in length 101239; gap of 100 bp 100 bp 1013810; gap of 100 bp 113810; gap of 100 bp 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
rf 915 bp in length
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if 863 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
of 851 bp in length
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f 878 bp in length
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f 843 bp in length
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f 905 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910: contig of 910 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
914 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
f 883 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7847: gap of 100 bp 8755: contig of 908 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8855: gap of 100 bp 9753: contig of 898 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 100 bp contig of 904 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14784: gap of 100 bp 15662: contig of 878 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77: gap of 100 bp
17678: contig of 901 bp in length
78: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 92 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
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1011 1873; contig of 1874 1973; gap of 10
1974 2824; contig of
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3802: contig of
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4816: contig of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L4483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 24_J_9
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16677: cont.
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12840 13710: cont
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17679 17778: qap of
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6764: cor
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10757: cor
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31554 31553; gap of 100 bp 31554 32452; contig of 899 bp in length 31453 3252; gap of 100 bp 32453 3252; gap of 100 bp 33448 33547; gap of 100 bp 33548 33447; contig of 895 bp in length 33548 33547; gap of 100 bp 3553 gap of 100 bp 35534 3553; gap of 100 bp 3553 38502; gap of 100 bp 3553 38502; gap of 100 bp 35803 39380; contig of 880 bp in length 39480; gap of 100 bp 39481 4405; contig of 898 bp in length 40408 4550; gap of 100 bp 41506 4239; gap of 100 bp 41506 4239; gap of 100 bp 41506 43357; contig of 898 bp in length 41357; contig of 898 bp in length 41357; dap of 100 bp 4156 43357; contig of 899 bp in length 41357; dap of 100 bp 4156 41355; contig of 899 bp in length 41357; dap of 100 bp 4156 41355; contig of 899 bp in length 41357; dap of 100 bp 4156 41355; contig of 899 bp in length 41357; dap of 100 bp 4156 41565; gap of 100 bp 41566 41566; ga
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                                                        80 18779; gap of 100 bp 19532: contig of 853 bp in length 19732: gap of 100 bp 20634: contig of 902 bp in length 185 20734; gap of 100 bp in length 185 21720; contig of 886 bp in length 21 272579: contig of 859 bp in length 122579: contig of 859 bp in length
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23568: contig of 889 bp in length
23668: gap of 100 bp
24554: contig of 886 bp in length
24654: gap of 100 bp
25521: contig of 867 bp in length
18679: contig of 901 bp in length
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Best Local Similarity 99.1%; Pred. No. 3.5e-47;
Matches 216; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 6105 gap of 100 bp 1
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54325: gap of 100 bp
55206: contig of 881 bp in length
55306: gap of 100 bp
56165: contig of 859 bp in length
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Job time: 14005 sec
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| SIDS1/gcdata/hold-genessed/genessen-embl/NA1981_DAT:*
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Human polynucleoti
Human ABCAl homolo
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728.372 Million cell updates/sec
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                                                                                                                                                 September 20, 2002, 03:08:57; Search time 520.94 Seconds
                                                                                                                                                                                                                                                                                                          1 gtaattgcgagcgagagtga.....aacacaaaagtggaaaacag 22
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAI70315
AAF92831
AAH07432
AAH18606
AAH04729
AAH17451
AAK51683
ABA09200
                                                                                                 - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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## ALIGNMENTS

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Human; ATP binding cassette transporter 1; ABC1; coronary heart disease; dermatological, atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                    Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                                                                                                                                                                                     /product= "Human ABC1 protein"
                                                                                                                                                                                                Location/Qualifiers 321..7106
           AAD21326 standard; DNA; 7260 BP
                                                                                                                                                                                                                                                                                                              20-MAR-2000; 2000EP-0105820
                                                                                                                                                                                                                                                                                                                                     20-MAR-2000; 2000EP-0105820
                                                             28-JAN-2002 (first entry)
                                                                                                                                                                                                                          /*tag= a
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                               EP1136552-A1
                                    AAD21326;
AAD21326
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(FARB ) BAYER AG

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                                                                                                                                                                                      The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart diseases, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lbeta (IL-lbeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctc 67
                                                                                                                                                                                                                                                                                                                                                                    arthritis and septic shock. The present sequence is human ABC1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
501.7106
/*tag= b
/note= "alternative open reading frame of AAI70314"
                                                                                   New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholesterol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipaemic; antipsoriatic; dermatological; Tangler disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP binding cassette transporter 1; ABC1; human; lipid disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ATP binding cassette transporter 1 (ABC1) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 221; DB 22;
100.0%; Pred. No. 8.7e-55;
ilve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 221; Conservative
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                                                                                                                                                       Example 1; Fig 1; 48pp;
 Bodzioch M;
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                                 WPI; 2001-640388/74.
P-PSDB; AAE13022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Schmitz G,
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The present sequence is that of cDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AAM50227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAT70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 N-terninal amino acids to the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in Cifferent Tangier kindreds. In the variant genes (numbering as in AAT70314), G is changed to A at position 596, T is changed to C at position 1136, A is changed to G at position 2589 or G is changed to C at position 136, A is changed to G at position 3456, or any combination of these. All of these polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G) are both associated with a decreased in vitro ApoA-I mediated efflux of cholesterol from monounclear phagocytes, a feature typical of Tangier disease. 3 of the variants (G596A) are hothy and disease. All disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular diseases, and inflammatory diseases (CHD) relative to CHD-free control subjects. The use of the provided ABC1 transcribts or criterias by antisense or ribozyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         getttgeteettgtttttteeeeggttetgtttteteeeetteteeggaaggettgteaa 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 221; DB 22;
100.0%; Pred. No. 8.7e-55;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 26-28; 41pp; English.
                                                     /*tag= e
replace(3836,C)
eplace(1516,C)
                                       replace(2969,G)
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Matches 221; Conservative C
                                                                                                                                                                                                                 24-MAR-2000; 2000EP-0106401.
                                                                                                                                                                                                                                                        24-MAR-2000; 2000EP-0106401
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                                                                                                                                                                                                                                                                                                                                     Schmitz G, Bodzioch
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                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAM50228.
                                                                                                                                       EP1136554-A1
                                                                                                                                                                            26-SEP-2001.
    variation
                                         variation
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Gaps

128

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181 ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221

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AAH07432 standard; cDNA; 736

AAH07432 RESULT

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens. EP1074617-A2.

Human cDNA clone (5'-primer) SEQ ID NO:4267.

(first entry)

26-JUN-2001

AAH07432;

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28790 gtaattgcgagcgagagtgggtggggccgggacccgcagagccgagcccttctctc 28849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or KXR-mediated transcriptional activity or ABCl expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
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Pred. No. 3.1e-54;
1; Mismatches 0; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
                              181 ggggtaggagaagagacgcaaacacaaaagtggaaaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 1; 317pp; English.
                                                                                                                                                                                                     AAF92831 standard; DNA; 183999
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99.5%;
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2000US-0213958
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15-MAR-2000;
23-JUN-2000;
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AAF92831
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99JP-0248036. 99JP-0300253. 2000JP-0118776. 2000JP-0183767.

11-JAN-2000; 02-MAY-2000; 09-JUN-2000;

29-JUL-1999; 27-AUG-1999; (HELI-) HELIX RES INST

28-JUL-2000; 2000EP-0116126

07-FEB-2001

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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence of an oligonucleotide which comprises a 3'-end sequence. Or complementary to a polynucleotide which comprises at 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the cetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03628 and AAH13623 represent human amino acid sequences; and AAH13629 to AAH13622 or AAH13623 conservation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiyama T, Wakamatsu A, Nagai K,
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28910 gctttgctccttgtttttccccggttctgttttccccttctccggaaggcttgtcaa 28969

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                  ggggtaggagaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 18808; 2537pp + CD ROM; English.
No. 1.3e-54;
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A, Nagai K,
               0; Mismatches
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 Pred.
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Sugiyama T, Wakamatsu
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27-AuG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
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                 220; Conservative
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Best Local Similarity
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Ishii S,
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               Matches
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AAH18606
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13639 to AAH13629 and AAH13639 represent human cDNA sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                      121 getttgetecttgtttttteeeeggttetgtttteteeeetteteeggaaggettgteaa 180
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                                                                                                                                                                                                   Score 219.4; DB 22; Length 1556; Pred. No. 1.6e-54;
                                                                                                                                                                                                                                   1; Indels
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                                                                                                                                                        Sequence 1556 BP; 380 A; 363 C; 399 G; 414 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 1564; 2537pp + CD ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA clone (5'-primer) SEQ ID NO:1564.
                                                                                                                                                                                                                                   Mismatches
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99.5%;
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99JP-0300253.
2000JP-0118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000JP-0241899
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                                                                                                                               of the present invention.
                                                                                                                                                                                                                                      Matches 220; Conservative
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                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH04729;
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the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length coNas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length coNas. The primers allow obtaining of the full-length coNas assily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of a polynucleotide which comprises one of aligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the oplynucleotide which comprises a 3'-end sequence, where the oplynucleotide which comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
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Sequence 763 BP; 137 A; 205 C; 260 G; 158 T; 3 other;

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                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                          182
                                                                                                      gggetgeggeagggeagggeggggggetcegegeaceaacagageeggttetcagggege 122
                                                                                                                                61 gggctgcggcagggcagggcggggggggctccgcgcaccaacagagccggttctcagggcgc 120
                                                                                                                                                                                  121 tttgeteettgtttttteeeeggttetgtttteteeetteteceggaaggettgteaagg 180
                         0; Gaps
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                                                   3 aattgcgagcgagggggggggggggggggccgcagagccgagccgaccttctctccc 62
                                                                                                                                                          123 tttgetcettgttttttceceggttetgtttttcececttetceggaaggettgtcaagg
                                                                             1 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccttctcccc
99.1%; Score 219; DB 22; Length 763; 100.0%; Pred. No. 1.7e-54;
                         Indels
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        100.0%; Preu. ....
                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:16905
                                                                                                                                                                                                                                                                                                     AAH17451 standard; cDNA; 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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            Best Local Similarity 100.0
Matches 219; Conservative
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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  Query Match
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptises: (a) an oilgo-dT primer and an oilgouncleotide complementary to the complementary strand of a polyuucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oilgonucleotide comprises a sequence complementary to the complementary strand of a polyuucleotide which comprises a 5'-end sequence and an oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence of an oilgonucleotide which comprises a 3'-end sequence. Where the oilgonucleotide which comprises a 1'-end sequence of sequence of sequence of a polynucleotide which comprises as 1'-end sequence of the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the cDNAs are also without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH13631 represent human amino acid sequences; and AAH13629 to AAH13632 to Febresent plumers all of which are used in the exemplification of the borneant inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gggctgcggcagggcagggcgggagctccgcgcaccaacagagccggttctcagggcgc 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 aattgcgagcgagagtgagtgggccgggacccgcagagccgagccgtctctccc 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 aattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctccc 60
                                                            Yamamoto J;
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                                                         Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.1%; Score 219; DB 22;
100.0%; Pred. No. 2.2e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 219
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                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 16905; 2537pp + CD ROM; English.
                                                                                Wakamatsu A, Nagai K,
                                                            Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK51683 standard; cDNA; 7281 BP.
                                                            Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
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Matches 219; Conservative
               (HELI-) HELIX RES INST.
                                                                                    Sugiyama T,
                                                                                                                          WPI; 2001-318749/34.
                                                         Isogai T,
                                                                                                                                                                                                                                   full-length cDNAs
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                                                                                Ishii S,
                                                            Ota T,
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM88323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or eptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity insue growth factor activity, immunomodulatory activity and extivity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1086~1096; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2000; 20000S-0623325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-065851.
20-0CT-2000; 2000US-0633325.
30-NOV-2000; 2000US-0728422.
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2000US-0598075.
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                                                                                                                                                                                                                    WO200157190-A2.
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20-JUN-2000;
19-JUL-2000;
                                                                                                                                                  Homo sapiens.
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                                                                                                       Gaps
                                                                                                                                                                         36 cgatttcgtgtgtgtgtggggccgggacccgcagagccgagccgaccttctctcccgggct 95
                                                                                                                                      8 cgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccgggct 67
                                                                                                       ;
0
                                                         93.2%; Score 206; DB 22; Length 7281; 97.7%; Pred. No. 2.1e-50;
Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
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                                                                                                 0; Mismatches
                                                                                                 Conservative
                                                                              Similarity
                                                                              Best Local Sim:
Matches 209;
                                                         Query Match
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; brombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; oronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasculopic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                    Human ABCAl homologue-encoding cDNA, SEQ ID NO:976.
           ABA09200 standard; cDNA; 7086 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US03800.
                                                          11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                     WO200157188-A2.
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                    ABA09200;
ABA09200
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Sequences ABA00924 represent 1330 mover numeral purpreparates, and sequences ABA00924 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides of producing the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the collypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth activity; considered activities; cemporal activities; hemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Compending on their biological activities; polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions e.g., by protein or gene therapy. Such conditions include conditions e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., mayeloid or lymphoid cell alsomator, cancers, haematopoletic disorders (e.g., asthma or arthritis), atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammallan subject

Claim 1; Page 833-835; 1963pp; English.

e.g. arthritis and cancer

2001-457740/49.

P-PSDB; ABB11956,

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vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of virah, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 ggcagggcgggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgt 124
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                                                                                                                                                                                                                                                                                                       22; Length 7086;
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0
                                                                                                                                                                                                                                                     Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
                                                                                                                                                                                                                                                                                                     Query Match 92.9%; Score 205.4; DB 22; Length Best Local Similarity 99.5%; Pred. No. 3.2e-50; Matches 206; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Drmanac RT, Asundi V, Zhou P,
                                                                                                                                                                                                                    novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 agacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 agacgcaaacacaaaagtggaaaacag 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 2196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK52667 standard; cDNA; 7086
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2000US-0598075.
2000US-0620325.
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2000US-0693325.
2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0496914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000;
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, memanatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                              (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 ggcagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctcttgt 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ggcagggcgggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgt 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 gagtgagtgggggccgggacccgcagagccgagccgaccttctctcccggggctgcggcag 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 205.4; DB 22; Length 7086; pred. No. 3.2e-50; 0; Mismatches 1; Indels 0;
 Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
Wang D, Wang J, Zhang J, Ren F, Chen R,
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human ABC1 protein"
                                                                                                                                                  Claim 1; Page 4558-4560; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 agacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 agacgcaaacacaaaagtggaaaacag 211
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298..7078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ABC1 DNA sequence #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                  WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                    P-PSDB; AAM79534
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                                                                                                                                                                                                                                                                                                                                                      inflammation
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     Zhao QA,
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                    Xue AJ,
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Matches
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                                                                                                                                                                                                                   The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                 Naudin L;
                                                                                                          Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cagggcgggggggctccgcgcaccaacagagccggttctcaggggcgctttgctccttgttt 136
                                                                                                                                                                                                                                                                                                                                                                                                                      17 gtgagtggggccgggacccgcagagccgagccgaccttctccccggggctgcggcaggg 76
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                             Rosier-Montus M, Arnould-Reguigne I, Prades C,
Duverger N, Jaye M, Searfoss GH, Remaley A, B
                                                                                                                                                                                                                                                                                                                                                                                Length 9854;
                                                                                                                                                                  New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                              92.8%; Score 205; DB 22;
100.0%; Pred. No. 4.6e-50;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 13690.
                                                                                                                                                                                                  Claim 1; Page 209-213; 368pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 acgcaaacaaaagtggaaaacag 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                     26-OCT-2000; 2000WO-EP10886.
                                                  01-MAR-2000; 2000US-0186260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC09615 standard; cDNA; 227
                                          99EP-0402668
                                                                       (AVET ) AVENTIS PHARMA SA.
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                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 205; Conservative
                                                                                                                                   WPI; 2001-316327/33.
                                                                                                                                                 P-PSDB; AAU02176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5' EST;
                                          26-OCT-1999;
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 03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                             Denefle P,
Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                Duery Match
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                                                                                                                   Dean M;
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 ccgggctgcggcagggcagggcgggggggctccgcgcaccaacagagccggttctcagggc 150
                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ccgggctgcggcagggcagggcgggggggggccgcccaacagagccggttctcagggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 getttgeteettgtttttteeeeggttetgtttteteeeetteteeggaaggettgteaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 3.1e-48;
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                                                                                                                                                                                                                                                   Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 13690; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.1%; Scor.
100.0%; Pred. No. 5.-
... 0; Mismatches
                                                                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression and secretion vectors.
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                                                          21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
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Best Local Similarity
                                                                                                                                                                                     (GEST ) GENSET
06-SEP-2000
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AAF24702;
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binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
membranes and utilises ATP hydrolysis to transport a wide variety of
membranes and utilises ATP hydrolysis to transport a wide variety of
ubstrates across the plasma membrane. ABC1 is a pivotal protein in
the apolipoprotein-mediated mobilisation of intracellular cholesterol
stores. ABC1 is defective in Tangier disease, a genetic disorder
characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
localised to chromosome 9422-9431. The ABC1 genes and proteins are
useful for developing pharmaceutical agents for the treatment of heart
disease and other disorders associated with hypercholesterolemia and
atherosclerosis. The genes are useful for developing screening assays to
screen for compounds that regulate the expression of genes associated
with cholesterol transport. The genes and proteins are also useful for
the disorders associated with hypercholesterolemia.
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                                                                                                                                                                                                                                                                                                                                                                Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gttctgttttctccccttctccggaaggcttgtcaaggggtaggagaaagagacgcaaac 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                            /product= "ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 122-128; 215pp; English.
                        Location/Qualifiers
291..7076
/*tag= a
                                                                                                                                                                                                        99US-0140264.
99US-0153872.
99US-0166573.
                                                                                                                                                                                                                                                                                                      Wade D, Garvin M;
                                                                                                                                                                          16-JUN-2000; 2000WO-US16765
                                                                                                                                                                                                                                                                       (CVTH-) CV THERAPEUTICS INC.
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Best Local Similarity 100.0
Matches 197; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis
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   Homo sapiens.
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AAF24702 standard; DNA; 10442 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggagetccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttccccg 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
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100.0%; Pred. No. 1e-47;
tive 0; Mismatches 0; Indels 0;
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                                                             Nucleotide sequence of a human ABC1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "ABC1 polypeptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 117-123; 211pp; English
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
291..7076
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(first entry)
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Best Local Similarity
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Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

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Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
61 ggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttccccg 120
                   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                   Human; adenosine triphosphate binding cassette protein 1; ABC1; applipoprotein-rediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9411; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                /product= "defective ABC1 polypeptide"
                                                                                                                                                                                                                                                                     Location/Qualifiers 323..7108
                                                                                                                           AAF24685 standard; DNA; 10474 BP.
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The present sequence encodes a human adenosine triphosphate (ATP)
binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangier disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangier disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hyperchlosterolemia and atherosclerosis. The
genes are useful for developing screening assays to screen for compounds
that regulate the expression of genes associated with cholesterol
transport. The genes and proteins are also useful
scorniated with hymorphylogical disease and other disorders
associated with miscellular disease and other disorders

associated with hypercholesterolemia.

Disclosure; Page 148-154; 215pp; English.

atherosclerosis

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                                                                                                                                               76 gcagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgtt 135
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                                                                        16 agtgagtggggccgggacccgcagagccgagccttctctccccgggctgcggcagg
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     Length 10474;
                                        10; Indels
   Score 190; DB 22;
Pred. No. 1.1e-45;
                                      0; Mismatches
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Job time: 10625 sec
                                                                                                                                                                                                                                                                                                                       204 gacgcaaacacaaaagtggaaaacag 229
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vuery Match 86.0%;
Best Local Similarity 95.1%;
Matches 196; Conservative
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Page 11

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 03:21:31; Search time 110.16 Seconds

(without alignments)
492.783 Million cell updates/sec

Title: US-09-846-456-4

Sequence: 1 graattgcgaggaggtga.....aacacaaaagtggaaaacag 221

Scoring table: IDENTITY_NUC
Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Listing first 45 summari Database : Issued Patents NA:\*

issued\_patents\_NA:\*

1: \cgqu2\_6\ptodata/2/lna/5A\_COMB.seq:\*
2: \cgqu2\_6\ptodata/2/lna/5B\_COMB.seq:\*
3: \cgqu2\_6\ptodata/2/lna/6A\_COMB.seq:\*
4: \cgqu2\_6\ptodata/2/lna/6B\_COMB.seq:\*
5: \cgqu2\_6\ptodata/2/lna/FB\_COMB.seq:\*
6: \cgqu2\_6\ptodata/2/lna/PCTUS\_COMB.seq:\*
6: \cgqu2\_6\ptodata/2/lna/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 7, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli	H H H H H H H H
SUMMARIES	US-09-191-171-7 US-09-191-171-7 US-09-191-171-7 US-08-327-832-4 US-08-327-832-4 US-09-191-171-4 US-09-191-171-4 US-09-185-707-4 US-09-185-972A-3 US-08-745-880-3 US-08-745-880-1 US-09-568-102-1 US-09-568-102-1 US-09-568-480-1 US-09-568-472-1 US-09-568-472-1 US-09-568-472-1 US-09-568-472-1	PCT-US95-11869-1 US-08-793-035-3 US-09-429-322-3 US-08-125-468-1 US-08-474-933-1 US-09-103-840A-2 US-09-103-840A-1
DB		200444 44
Length	4480 4480 3509 3509 2067 21155 2155 2255 4405 68750 68750 68750 68750 68750 68750 68750 68750	1809 1299 2754 30001 30001 4403765
% Query Match		13.1 13.1 13.1 13.0 13.0
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CLASSIFICATION:

PULGASJII/CATION DATA:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/494,104
FILING DATE: 2 - JUN-1995
APPLICATION NUMBER: AU PK9490/91
FILING DATE: 14-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU92/00611
FILING DATE: 12-NOV-1992
APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-JUL-1993
ATPOREZ/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANGE: 516-742-4343

15-559-2 Sequence 2, Appli C-474-2 Semisore 2 anni	Seguence 2.	Sequence 5.	1 Sequence 1,	Sequence 1,	Sequence 1,	Sequence 5,	Sequence 3,	Sequence 3,	Sequence 5,	Sequence 5,	.42 Sequence 42,	.42 Sequence 42,	-510-42 Sequence 42,	75 Sednence 47	42 Sequence 4	MENTS												ALPHA-L-IDURONIDASE AND GENETIC	TING SUIT		PRESSER									Version #1.25		
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28.6	28.6	28.6	28.4	28.4	28.4	28.2	28.2	28.2	28.2	28.2	28.2	7.87	7.87	200	28.2		-	171 770	e 7, Apr No. 6149		GENERAL INFORMATION:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	S C	R OF	CORRESPONDENCE ADDRESS	ADDRESSEE:	 H	CITY: Gar	STATE: Ne	. KY :	ZIF: II530	MEDITIM TVDE	COMPUTER	OPERATING SYSTEM:	SOFTWARE:	CURRENT APPLICATION DATA:	GOOD TOWNSON WITHOUT TOOK
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APPLICANT: SCOTT, Hamish S.
APPLICANT: ORSBORN, Donald S.
APPLICANT: ORSBORN, Annette M.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: HOPWOOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC TITLE OF INVENTION: SEQUENCES ENCODING SAME
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                                                                                                                                                                                                                                                       Query Match 13.9%; Score 30.8; DB 3; Length 4480; Best Local Similarity 53.3%; Pred. No. 6.4; Matches 65; Conservative 0; Mismatches 57; Indels 0;
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PatentIn Release #1.0, Version #1.25
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STREET: 400 Garden City Plaza
CITY: Garden City
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REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8978;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09385707; Patent No. 6238662
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-191-171-7
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-385-707-7/c
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APPLICANT: Ono, Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
TITLE OF INVENTION: Retroviral Expression Contructs Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                2775 TGGAACCCCGGCTTACCCGGGCGGGGGGGCACCCCGCGCAGCCGCAGCGTCACCGCGACG 2716
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                                                                                                                                                                                                                                                                                                                                                        66 ctgcgggcagggcaggggggggggctccgcgccaacaacagagccggttctcagggcgctt 125
                                                                                                                                                                                                                                                             6 tgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccggg 65
                                                                                                                                                                                                             ..
                                                                                                                                                          Query Match 13.9%; Score 30.8; DB 4; Length 4480; Best Local Similarity 53.3%; Pred. No. 6.4; Matches 65; Conservative 0; Mismatches 57; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: POSOTSKE, LAUTENCE H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.46362
TELECOMUNICATION INFORMATION:
TELEPAX: 20-2 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08327832
Patent No. 5840832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
                                                     , MOLECULE TYPE: DNA (genomic) US-09-385-707-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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LENGTH: 3509 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                      single
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STRANDEDNESS: doub
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
TYPE: nucleic acid
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                                             linear
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                    STRANDEDNESS:
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US-08-327-832-4
                                             TOPOLOGY:
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                                                                                                                                                                    Query Match
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RESULT
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                                                                                                       2581 AGGGTGAGCTGGTATGGCAGGGTGCCATACAGGGGTGCCCACAGTCAGCTCTGGGGGTGG 2522
                                                                                                                                                                         2521 TGCAGGGCTGCTTGCAGGGCTCATCCACAAGACACTCCCCTTTGTGACAGAGTCTCTGAC 2462
                                                                                                                                         70 ggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctc 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                        13.8%; Score 30.6; DB 2; Length 3509; 51.9%; Pred. No. 6.7;
Score 30.6; DB 2; Length 3509;
Pred. No. 6.7;
0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: POSOTSKe, Laurence H.
REGISTRATION NUMBER: 34,698
REFRENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
                                                                                                                                                                                                                                                                                                           US-08-828-584-4/c
; Sequence 4, Application US/08828584
; Patent No. 5908762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1001 G Street, N.W. CITY: Washington, D.C. STATE: District of Columbia COUNTRY: U.S.A.
     Query Match 13.8%;
Best Local Similarity 51.9%;
Matches 69; Conservative
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Matches 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3509 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                             2461 ATTTGTGCATCCC 2449
                                                                                                                                                                                                            130 cttgttttttccc 142
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CLASSIFICATION: 435
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US-08-828-584-4
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                                               2521 TGCAGGGCTGCTTGCAGGGCTCATCCACAAGACACTCCCCTTTGTGACAGAGTCTCTGAC 2462
70 ggcagggcagggcggggggggctccgcgcaccaacagagccggttctcagggcgctttgctc 129
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                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: RADIN, DAVID N.
APPLICANT: CRAMEN, CAROLE L.
APPLICANT: WEISSENBORN, DEBORAH L.
APPLICANT: WEISSENBORN, DEBORAH L.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1340 cGGGTGTCGTCGCTCGCGTAGATCAGCACCGCGGCGCGCCCAGGC 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,928B
FILING DATE: 13-SEP-1996
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 60/003,737
FILING DATE: 14-SEP-1995
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30.4; DE
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 7956-0011-999
ELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 669-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                        US-08-713-928B-8/c
; Sequence 8, Application US/08713928B
; Patent No. 5929304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.8%;
55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                             2461 ATTTGTGCATCCC 2449
                                                                                                  130 cttgttttttccc 142
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-713-928B-8
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1428 CGGGTGTCGTCGCTCGCGTAGATCAGCACCGCGGCGCGCCCAGGC 1385
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/494,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUBBER: 31,346
REFERENCE/DOCKET NUBBER: 89782
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFA: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2155 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                       US-09-385-707-4/c; Sequence 4, Application US/09385707; Patent No. 6238662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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US-09-385-707-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-871-572B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                         APPLICANT: SCOTT, Hamish S.
APPLICANT: ANSON Donald S.
APPLICANT: ANSON Donald S.
APPLICANT: ORSBORN, Annette M.
APPLICANT: ORSBORN, Annette M.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: HORRIS, Charles P.
APPLICANT: HOWGRIS, Charles P.
APPLICANT: HOWGRIS, Charles P.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
TITLE OF INVENTION: SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 30.4; DB 3; Length 2155; 55.8%; Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PUBLICATION NUMBER: US 08/494,104
FILING DATE: 13-JUN-1995
APPLICATION NUMBER: US 08/091
FILING DATE: 14-NOV-1991
PRIOR APPLICATION DATA:
FILING DATE: 10-NOV-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-JUN-1993
APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-JUL-1993
APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-JUL-1993
APPLICATION NUMBER: B978Z
FREERENCE/DOCKET NUMBER: 8978Z
TELEPHONE: 316-742-4366
TELEPHONE: 316-742-4366
TELEPHONE: 316-742-4366
TELEPHONE: 316-742-4366
TELEPHONE: 310-742-4366
TELEPHONE: 2155 DASE PAIRS
TELEPHONE: S16-742-4366
TELEPHONE: 2155 DASE PAIRS
TELEPHONE: S16-742-4366
TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: SCULLY SCOTT MURPHY & PRESSER : 400 Garden City Plaza Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                      Sequence 4, Application US/09191171
Patent No. 6149909
Patent No. 6149909 6143294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.8
Matches 58; Conservative
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; LOCATION: 89..2047
US-09-191-171-4
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                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
US-09-191-171-4/c
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1488 GGGCGGGGGGCACCCGCGCAGCGTCACCGCGACGTTGCGGTTGGGGTGGGCG 1429
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gggccgggacccgcagagccgagccgaccttctctcccgggctgcggcagggcg 83
GENERAL INFORMATION:
APPLICANT: SCOTT, Hamish S.
APPLICANT: OKSBORN, Annette M.
APPLICANT: OKSBORN, Annette M.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: CLEMENTS, Charles P.
APPLICANT: MORRIS, CHARLES P.
APPLICANT: MO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SCULLY SCOTT MURPHY & PRESSER 400 Garden City Plaza
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TELECOMMUNICATION INFORMATION:
TELEPRAX: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4405 base pairs
                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON & HOWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACID
EDNESS: double
                                                                                                                                            STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408..2789
                                                                                                                         Spring House
  TITLE OF INVENTION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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; LOCATION:
US-07-885-972A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 ggggccgggacccgcagagccgagccgaccttctctcccgggctgcgggcagggcaggc 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.4%; Score 29.6; DB 4; Length 2255; Best Local Similarity 61.8%; Pred. No. 11; Matches 47; Conservative 0; Mismatches 29; Indels 0
                                                                                               APPLICANT: SOCIAL AND JUST APPLICANT: SOCIAL APPLICANT: Donnelly, Robert APPLICANT: Mariano, Thomas APPLICANT: Cock, Jeffrey APPLICANT: Emmanuel, Stuart APPLICANT: Schwartz, Barbara TITLE OF INVENTION: Accessory Factor for Interferon Gamma TITLE OF INVENTION: and its Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/871,572B
FILING DATE: 9-UNE-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barr, Philip J.
Brake, Anthony J.
Kaufman, Rnadal J.
Tekamp-Olson, Patricia
Waaley, Louise
Wong, Polly A.
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; Sequence 3, Application US/07885972A
; Patent No. 5460950
Sequence 3, Application US/08871572B Patent No. 6287853
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: 758 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MUCCION, RICHARD R.
REGISTRATION NUMBER: 32,538
REFERENCE/POCKET NUMBER: UMD1-
TELECOMMUNICATION INFORMATION:
TELEFHONE: (908) 273-4988
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE.

LENGTH: 2255 Dase Fr.

TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                         Pestka, Sidney
Kotenko, Serguei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 GGGAAGAGCGGGCCC 540
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                                                                                                                                                                                                                                                                                                             ADDA...
STREET: 755
CITY: Summit
TIP: New Jersey
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Barr, F
APPLICANT: Brake,
                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 07901
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US-08-871-572B-3
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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7 gcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccgggc 66
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Expression of PACE in Host Cells and
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                     ADDRESSEE: Howson & Howson
STREET: Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 tgcggcagggcagggcggggggggcgcgcaccaacagag 106
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,972A
FILING DATE: 19920520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION PATA:
APPLICATION NUMBER: US 07/621,092
FILING DATE: 26-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,859
FILING DATE: 29-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,443
FILING DATE: 29-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,445
FILING DATE: 30-NOV-1990
ATORNEY AGENT INFORMATION:
NAME: Bak, Mary E.
RESISTRATION NUMBER: 31,215
RESISTRATION NUMBER: GIS181A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08745880
Patent No. 5965425
GENERAL INFORMATION:
APPLICANT: Barr, Philip J.
APPLICANT: Brake, Anthony J.
APPLICANT: Texamp-olson, Patricia
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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275 GCTCGGGAGGGTGAAGAGTGCCGACCCCTGGGGAGCCCTGGCGGGAAACTTTTCCAGGC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 gcgagcgagagtgagtggggccgggacccgcagagccgagccgaccttctctcccgggc 66
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APPLICANT: Wasley, Louise
APPLICANT: Wong, Polly A.
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Methods of Use Thereof
                                                                                                                                                                               Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                  ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/480,382
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 07/621,092
FILING DATE: 26-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,493
FILING DATE: 29-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,443
FILING DATE: 29-NOV-1990
PRIOR APPLICATION NUMBER: US 07/621,443
FILING DATE: 30-NOV-1990
PRIOR APPLICATION NUMBER: US 07/621,443
FILING DATE: 30-NOV-1990
ATTORNEY APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-NOV-1990
ATTORNEY APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-NOV-1990
ATTORNEY APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/745,880
FILING DATE: 08-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GI5181A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON & HOWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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56.0%;
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LENGTH: 4405 base pairs
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Best Local Similarity 56.05
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                               Spring House
Pennsylvania
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408..2789
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US-08-745-880-3
                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 4405;
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Pred. No. 14;
0; Mismatches 44; Indels
GENERAL INFORMATION:

APPLICANT: Bark, Philip J.

APPLICANT: Brake, Anthony J.

APPLICANT: Kaufman, Rnadal J.

APPLICANT: Kannp-Olson, Patricia

APPLICANT: Wasley, Louise

APPLICANT: Wong, Polly A.

APPLICANT: Wong, Polly A.

TITLE OF INVENTION: Expression of PACE in Host Cells and

TITLE OF INVENTION: Methods of Use Thereof
                                                                                                                                                                                                                                                                                        STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,382
FILING DATE: US/08/480,382
FILING DATE: US/08/480,382
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 07/485,972
FILING DATE: 20-MAY-1992
APPLICATION NUMBER: US 07/621,092
FILING DATE: 26-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,859
FILING DATE: 25-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,443
FILING DATE: 25-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,443
FILING DATE: 25-NOV-1990
PRIOR APPLICATION NUMBER: US 07/621,445
FILING DATE: 25-NOV-1990
PRIOR APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-NOV-1990
ATTONIEV/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                    Howson & Howson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO: 3:
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TYPE: nucleic acid
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Best Local Similarity 56.08
Matches 56; Conservative
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                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson & I
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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408..2789
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Sequence 3, Application US/08480382

RESULT 11 US-08-480-382-3/c 

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                                                                                 APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Girkle, Ross
APPLICANT: Granden, Joern
APPLICANT: GPRIDACH, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 30
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERENCE: 4.30582A
CURRENT FILING DATE: 2000-05-10
PRIOR FILING DATE: 1099-06-17
PRIOR FILING DATE: 1099-06-17
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.8%; Pred. No. 35;
Matches 47; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.4%; Score 29.6; DB 4; Length 68750; Best Local Similarity 61.8%; Pred. No. 35; Matches 47; Conservative 0; Mismatches 29; Indels 0;
                     Sequence 1, Application US/09335409
Patent No. 6121029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09568102
Patent No. 6346404
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-335-409-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-102-1
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                                                                GENERAL INFORMATION:
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LENGTH: 68750
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JS-09-335-409-1
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APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Alvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Gyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
PRIOR PLILING DATE: 2000-05-10
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                   APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirtle, Ross
APPLICANT: Zirtle, Ross
APPLICANT: Gerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION UNIBER: US/09/567,969
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR PILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.0
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Best Local Similarity 61.8%; Pred. No. 35;
Matches 47; Conservative 0; Mismatches
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                                            Sequence 1, Application US/09567969
Patent No. 6355457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09568480 Patent No. 6355458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-480-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORGANISM: Sorangium cellulosum US-09-567-969-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 18370 cgatcggcgaggtgct 18385
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                                                                                                                  APPLICANT: Schupp, Thomas
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Best Local Similarity
                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 68750
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RESULT 14
US-09-567-969-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Search completed: September 20, 2002, 03:21:58 Job time: 14207 sec

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RESULT
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                                                ; Search time 5225.75 Seconds (without alignments) 636.716 Million cell updates/sec
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                                                                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                          1797656 seqs, 10463268293 residues
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                                                September 20, 2002, 03:14:51
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Maximum Match 100%
Listing first 45 summaries
                                - nucleic search, using sw model
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Perfect score:
Sequence:
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A75926 Mus musculu AB55982 Homo sapi AF362377 Gallus ga Continuation (9 of AL353725 Human DNA AC102919 Mus muscu AX092843 Sequence AX080494 Sequence

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AB055982

AF362377

AX092843 AF287142

AC102919

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AC073805 Mus muscu AF328787 Homo sapi

AF328787 Homo sapi AX320362 Sequence

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AF258627 Homo sapi AF258624 Homo sapi AX139751 Sequence AX252277 Homo sapi AX252377 Homo sapi AX25452 Sequence AX127830 Sequence AX139813 Sequence AX139813 Sequence AX139818 Sequence AX139818 Sequence AX13783 Homo sapi AK04328 Homo sapi AK037924 Homo sapi AK092594 Sequence AX137712 Sequence AX137712 Sequence AX137712 Sequence AX07344 Homo sapi

AX127831 AX139818 AL353685 AC012230 AF287262

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AX351033 AX351030 AX060713 AX060892 AF285167 AX060719 AX060721 AX060898

AX351033 AX351030 AX060713 AX060892 AF285167 AX060719 AX060721

AX060898 AX060900

Sequence Sequence

Sequence Sequence Sequence

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PAT 06-FEB-2002
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 5 08-Nov-2001;
Aventis Pharma S.A. (FR)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ALIGNMENTS
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AX351033
AX351033.1 GI:18616389
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Description

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10442)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Dene
Rever,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Brequlatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 2 08-NOV-2001;
Aventis Pharma S.A. (FR)
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nilarity 100.0%; Pred. No. 1.6e-33;
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Sequence 2 from Patent WO0183746.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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App binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 18-DEC-2000;
CV THERAPEUTICS, INC. (US)
Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abcl
Patent: WO 0078972-A 1 28-DEC-2000;
CV THERAPEDIUS, INC. (US)
Location/Qualifiers
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SOURCE

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GTEPARKRAFGDKQSCARFTEDDRADPWISDIDPESRFFDLLGSWOK
GWKLTQOQFVALLWRKLIARRSRKGFFAQIYLPAVFVCIALVFSI,TYPPEGYTYPSLE
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DAIKQMKKHIKLAKDSSADRFLNSLGFFWTGLDTRNNVKWWFNNKGWHAISSFLNVIN
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SQLSGGWRKELSVALAFVGGSKYVILDEPTAGVDPSRRGIUBELLKYKRGRTITILST
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PASFVVFLIQERVSKAKHLQFISGVKPVIYMLSNFVMDMCNYVVPATLVIIFICFQQ
KSYVSSTNLPVLALLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 10442)
                                                                                                                                                                                                                                                                                                                                                 Schwartz.K., Lawn,R.M. and Wade,D.P. ABCAl gene expression and apoA-I-mediated cholesterol efflux are
Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
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Lawn, Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J. G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Direct Submission
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/protein_id="AAF98175.1"
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/chromosome="9"
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/codon_start=1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abc1
Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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0; Mismatches 2;
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/db_xref="taxon:9606"
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1 (bases 1 to 10474)

Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.

Atp binding cassette transporter protein abc1 polypeptides Patent: WO 0078971-A 7.28-DEC-2000;

CV THERAPEUTICS, INC. (US)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10474)
Lawn, R.M., Wade, D. and Garvin, M.
Lawn, R.M., Wade, D. binding cassette transporter protein abcl Patent: WO 0078972-A 9 28-DEC-2000; CV THERAPEUTICS, INC. (US)
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/organism="Homo sapiens"
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PAT 22-JAN-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 GAGCCACACGCTGGGGTGGCTGGCTGGCTGAACATGGCTTGGCCTCAGCTGAGGTTG 349
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Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
Location/Qualifiers
1. .149034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 TTAATGACCAGGCCACGGGCGTCCCTGCTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCC 289
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Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
Atp binding cassette transporter protein abc1 polypeptides
Patent: Wo 00708971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Homo sapiens ABCAl (ABCAl) gene, complete cds.
AF275948
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Pred. No. 1.1e-32;
0; Mismatches 2;
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               DNA
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/db_xref="taxon:9606"
a 2304 c 2415 g 2844
Sequence 9 from Patent WO0078971.
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Best Local Similarity 98.77
Matches 157; Conservative
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mRNA

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25038. 25314

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25038. 25314

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142646. .142738,143397. .143640,144581. .144721)
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1454. .148034
/gene="ABCA1"
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11859. 12133
7.rpt_family="Alu"
12810. 12902
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DAXKQMKHLKLARDSSADREINSLGRPWTGLDTRNNYKVWFNNKGWHAISSFLNYIN
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SASFVVELIGERVSKAKLIGTSGVRYPVIMLERVTJIFFCRQQ
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LTGDTTVTRGDAFLNXNSILSNIHEVHONMGYCPQFDAITELLTGREHVBFFALLRGV
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVXKEKHRNMLQYQLPSSLSSLARI
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Homo sapiens
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Matches 155; Conserv
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JOURNAL
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AF258627
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Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M. Compositions and methods for modulating hdl cholesterol and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25831 TTAATGACCAGGCCACGGGGGGTCCCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCC 25890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             triglyceride levels
Patent: WO 0115676-A 1 08-MAR-2001;
University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                     ttaatgaccagccacggggtcctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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0; Mismatches 7.
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/db_xref="taxon:9606"
37944 c 41170 g 54950 t
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67123. .67382
/rpt_family="Alu"
68499. .68731
                                  /rpt_family="Alu"
55297. .55344
/rpt_family="Alu"
58501. .58935
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                                                                                           /rpt_family="HERV"
61246. .61480
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62812. .63077
/rpt_family="Alu"
64082. .64306
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72244. .72501
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69481. .69760
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 /rpt_family="Alu"
55029. 55000
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98.7%;
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Best Local Similarity 98.73
Matches 157; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

8 Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Analysis of hakel gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

L Biochem. Biophys. Res. Commun. 271 (2000) In press

E 2 (bases 1 to 697)

S Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Direct Submission

L Submitted (19 APR-2000) Cardiovascular Research Institute, University of California, San Francisco, C.A. 94143-0130, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens ATP binding cassette transporter 1 (ABCA1) mRNA, partial cds. AF258627
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/protein_id="AAF69513.1"
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/ranslation="MACWPQIRILL"
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Pred. No. 3.1e-29;
1; Mismatches 2;
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/db_xref="taxon:9606"
/chromosome="9"
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/gene="ABCA1"
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illarity 97.5%;
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Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene, exon
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                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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artificial sequence.
1 (bases 1 to 446)
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
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Pullinger C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Anoizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABCl gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Biochem. Blophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 200)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aquizerat, B.E., Fielding, C.J. and Kane, J.P.
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/db_xref="taxon:9606"
/chromosome="9"
/map="9431"
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1 (bases 1 to 446)

Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searfoss Iii, G.H., Remaley, A., Brewer, H.B. and Dean, M.

Nucleics acids of the human abcl gene and their therapeutic and diagnostic application

Adagnostic application

Patent: EP 1096612-A 3 02-MAY-2001;

Aventis Pharma S.A. (FR)

Location/Qualifiers
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Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H., Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abcl gene and their therapeutic and
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                                                                                                                                                                                         /organism="synthetic construct"
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/db_xref="taxon:32630"
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                                                                       diagnostic application
Patent: WO 0130848 A 3 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Sequence 3 from Patent EP1096012.
AX139751
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Db 212 CTGCTGTGGAAGAACCTCACTTTCAGAAGAAGAAGAACA 250

Search completed: September 20, 2002, 03:15:13 Job time: 14027 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

September 20, 2002, 01:23:14; Search time 3895 Seconds (without alignments) 765.809 Million cell updates/sec

1 gtaattgcgagcgagagtga.....aacacaaaagtggaaaacag 221 US-09-846-456-4 221 Title: Perfect score: Sednence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

27472414 13736207 segs, 6748477542 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AU135588 AU135588 AU121731 AU121731 Z44777 HSC12B0B1 IN BG678861 602644760 AZ76996 IM0571A17 BB657864 BB657864 BB65939 BB65939 BB594197 BB594197 BB594197 BB594265 BB594265 BB594265 BB594265 BB594265 BB594265 BB594265 BB570397 BB570397 BG58933 BB568933 BB570397 BB570397 BG584247 S03216 MAAAL053013 Drosophil BH470300 BOHMIG9TR AL053013 Drosophil BH470300 BOHMIG9TR AL209465 Tetracodon BB374442 BB374442
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C76305 AG127909		AG131276	CNS01677	AG137074	BB318923	BI101161	AI850822	AW489757	AW490154	BE948350	BB698363	BE943674			BB696895		BB547934	AG073892	æ	BE692826	BI082717	AA098273	BB790023	BF224565	BF319828	AA562016
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37.2	37	37	36.8	36.8	36.6	36.4	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36	35.6	35.6	35.6	35.6	35.6	35.6	35.6	35.6
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## ALIGNMENTS

AU135588 AU135588 74-OCT-2000 AU13588 PLACE1 Homo sapiens cDNA clone PLACE1002437 5', mRNA sequence.	A0135588.1 GI:10996127 EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	٠ بـ	HRI human cDNA project Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan	Tel: 81-438-52-3951 Fax: 81-438-52-3951 Fax: 81-438-52-395- Braail: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute	Location/Qualifiers  1. 736 /organis="Homo sapiens" /db_xref="taxon:9606" /clone="PLACE1002437" /clone_lb="PLACE1" /tissue_type="placenta" /note="Vector: pME188F13"	163 a 199 c 199 g 170 t 5 others
RESULT 1 AU135588 LOCUS DEFINITION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT		FEATURES SOUTCE	BASE COUNT

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61 GGGCTGCGGCAGGGCAGGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGC 120
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 763)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Tammancto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                 1 GTAGTTGCGAGCGAGCGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 60
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
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                        DB 9;
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100.0%; Pred. No. 6.9e-42;
iive 0; Mismatches 0;
                    99.3%; Score 219.4; DB 9 99.5%; Pred. No. 5.5e-42; tive 0; Mismatches 1
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205 c 260 g 158 t
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HRI human cDNA project
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Genomics Laboratory
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/dev_stage="3 months old"
/dev_stage="3 months old"
/dev_stage="3 months old"
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Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes Auffray, C., Behar, G., Bois, F., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani Kabaktchis, C. and Tessier, A. IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242377 244377 292 bp mRNA linear EST 14-NOV-
HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                    121 TITGCICCITGITITITCCCCGGITCIGITITCICCCCTTCICCGGAAGGCTTGTCAAGG 180
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Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lzb08
Seq primer: (-21)Ml3_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 tttgctccttgttttttccccggttctgtttttctccccttctccggaaggcttgtcaagg
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="c-1zb08"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c-1zb08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244377.1 GI:573506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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95277534
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 BG678861 998 bp mRNA linear EST 01-MAY-2001 602624760F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4749735 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10603 row: g column: 16
High quality sequence stop: 860.
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//lab_host="bfl10B (Tl phage-resistant)"
//lab_host="bfl10B (Tl phage-resistant)"
//lab_host="bfl10B (Tl phage-resistant)"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 998)
                                                              139 tccccggttctgttttctccccttctccgaaggcttgtcaaggggtaggaaagagc 198
61 CAGGGGGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGGGGCGCTTTGCTCCTTGTTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:4749735"
/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                          BG678861.1 GI:13910258
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Matches 194; Conservative
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// Arachinster 5. Coll Strain Allo Volud, in Treststall, Fr. // Arachinster 5. Coll Strain Allo Volud, in Treststall, Fr. // Arachinster 5. Male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil47321141gblAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
TRB. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
7
                                       GSS 16-FEB-2001
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Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly A., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
547 bp DNA linear GSS 16-FEB-20(
1M0571A17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0571A17 F, DNA sequence.
AZ769996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xrsef="taxon:10090"
/clone="wcC1M6571A17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: A column: 17
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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Location/Qualifiers
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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Leases I to 625)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koyaz, S., Matsuyama, T., Miyazaki, A., Momura, K., Ohno, H., Kouda Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Taqami, M., Taqawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Unpublished (2001)
                                                                                                                                                                                                                                                                          /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB665939 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230023K11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 185 c 173 g 134 t l others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   /db_xref="taxon:10090"
/clone="D230019D04"
/clone=lb="RIKEN full-length enriched, 12 days embryo eyeball"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ccgggctgcggcagggcagggcgggggagctccgcgcaccaacagagccggttctcagggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCGC-AAAGCIGGGCAGGGGGCGCCGCGGGACCCGCGCAACCACAGCCGGCTIGGGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.5%; Score 67.4; DB 9; 62.4%; Pred. No. 4.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                           /dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                             /tissue_type="eyeball"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB665939
BB665939.1 GI:16499572
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JOURNAL
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8. Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Ragami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKBN Mouse ESTS (Arakawa, T., et al. 2001)

Lupublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 1 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@goc.riken.go.jp,
URL:http://genome-res@goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
URL:http://genome.goc.riken.go.jp,
W. Konno, H., Okazaki, Y., Mayatsu, M., and Hayashizaki, Y. Itoh
W. Konno, H., Okazaki, Y., Miramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Wadahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
'S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB657864 RIKEN full-length enriched, 12 days embryo eyeball Mus
musculus cDNA clone D230019D04 5', mRNA sequence.
                                                                                                                                                                                                                                                           ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
                                                                                                                                        85 CAGCGC-AAAGCTGGGCAGGGGGCGCCGCGGACCCGCGCAACCACCGCGGTTGGGGA 143
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26 GTAATTCCGAGGGCGAGCGAG-CGGGCCGGGACCGGCAGAGCCCACTTCTCTCCGCGGCG 84
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                                                                                                                                                                                                                                                                                                                                                               ggggtaggagaagagacgcaaacacaaaagtggaaaacag 221
                                                                                                                                                                                                                                                                                                                                                                                                                          204 GGGGTAGGGAAAACAGACTCAAACAGCAAAGTGGAAAACAG 244
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1. .619
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TITLE JOURNAL COMMENT

source

FEATURES

3

Length 619; Indels

house mouse.

ORGANISM

SOURCE

REFERENCE AUTHORS

9

BB657864

DEFINITION

ACCESSION

VERSION KEYWORDS

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BB594197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (11), Ribata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length CDNA
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nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, L., Alzawa
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
M., Ronno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikwa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer \{5^{\prime}
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.rlken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, 2 days pregnant adult female oviduct"
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
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Hayashizaki, Y.
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Alzawa, K. Akahira, Kocentia, Sciniogiachi, Muliace, Miliace, Mili
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation
Carninci,P. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                120 TGCTCTGCTCCCTGTTTCCCCCCCACTTTTTTCTTCCCCTTTCTGGAAGGGTTTGTGCAGG 179
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/dev_stage="4 days neonate"
/lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamH1; cDNA library was
                                                                                                                                                                                                                                                                                                                                      180 GGTAGGGAAAACAGACTCAAACAGCAAAGTGGAAAACAG 218
                                                                                                                                                                                                                           183 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
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Contact: Yoshihide Hayashizaki
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp,
carninci.p., Nishiyama.y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 259)
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primed with a primer [5'
GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'],
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                   system. Genome Res. 9 (5), 463.470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                    /close_lib="RIKEN full-length enriched, 4 days neonate
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%; Score 57.8; DB 9; Length 259; 57.1%; Pred. No. 0.00086; Live 0; Mismatches 92; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 ggtaggagaaagagacgcaaacacaaaagtggaaaacag 221
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/dev_stage="4 days neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="B630007C24"
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us-09-846-456-4.std.rst

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Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishii, Y., Itoh, W., Izawai, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sasaki, D., Safo, K., Shibata, K., Shibata, Y., Shinaqawa, A., Takahashi, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Watahiki, A., Yamamura, T., Yasunishi, R., Yoshida, K., Yikima, W., Willi, A., Wamanatsu, M. and Haysshizaki, Y.

FIKEN Mouse ESTS (Alzawa, K. et al. 2000)

Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Y. Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
'N., Okazaki,Y., Muramatsu,M. and Haysshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, 17 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.rtc.riken.go.jp) for
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/dev_stage="17 days embryo"
/lab_host="DH10B"
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Location/Qualifiers
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                                                                                    (bases 1 to 272)
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1; Gaps

25.0%; Score 55.2; DB 9; Length 272; 58.0%; Pred. No. 0.0035; Live 0; Mismatches 83; Indels

Conservative

Query Match Best Local Sim Matches 116;

Similarity

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 276)
Aizawa, K., Akahira; Akanira, T., Akanira, Y., Kaninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Harozane, T., Hodoyama, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Sakai, K., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Toya, T., Watamatsu, M. and Hayashizaki, Y. Yasunishi, A., Yoshida, K., RIKEN Mouse ESTS (Aizawa, K. et al. 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
A., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), $20-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
X., and Hayashizaki,Y.
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Schorest For Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="RIKEN full-length enriched, 1 day pregnant
adult female mammary gland"
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Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                        cggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttcc 141
                                                                                                                                                                                          79 GCCGCCGCGGGACCCGCGCAACCACAGCCGGCTTGGGGGAACTGCTCTGCTCTCTTTCC 138
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                                                         142 ccggttctgttttctccccttctccggaaggcttgtcaaggggtaggagaagagacgca
tggggccgggaccgcagagccgagccgaccttctctcccgggctgcggcagggcaggg
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details.
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KEYWORDS
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BB570397
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The bases 1 to 535)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. Design and Weele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
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single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                             /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 tttgctccttgttttttccccggttctgttttctccccttctcccggaaggcttgtcaagg 182
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303216 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
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PO Box 166, Clay Center, NE 68933-0166, USA
                  /tissue_type="mammary gland"
/dev_stage="1 day pregnant adult"
/lab_host="DH10B"
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Tel: 402 762 4366
Fax: 402 762 4390
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                        /tissue_type="pooled"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pGW SPORT6; Site_1: XbaI; Site_2: XhoI;
/note="Vector: pGW SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
I (bases 1 to 925)
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                                                                                             Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. .535
                                                                                                                                                                                       /organism="Sus scrofa"
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/clone_lib="MARC 1PIG"
                    FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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BOHMI69TR BOHM Brassica oleracea genomic clone BOHMI69, DNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
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Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSS: BOHMI69TF
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Fax: 301-838-0208
                                                                                                                                                                                      511 others
                                                                                                                                                                                                                                                                                                            e8; Indels
                                                                             /organism="Drosophila melanogaster"
/db_xxef="Laxon:7227"
/clone_lib="RPCI:98"
/clone="BACR19D16"
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/organism="Brassica oleracea"
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17.2%; Pred. No. 18;
tive 86; Mismatches
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/clone="BOHM169"
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Best Local Similarity 17.2%
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When : WWW.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Gistlute in Buffalo, NY. The library is named RCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                      Gaps
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 910)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
    Score 38.8; DB 12;
Pred. No. 23;
0; Mismatches 97;
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18.9%; Pred. No. 28;
tive 80; Mismatches
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Eukaryota; Metazoa; Arth
       17.6%;
50.0%;
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Query Match
Best Local Similarity 50.09
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Search completed: September 20, 2002, 01:23:18 Job time: 7378 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                    1736436 seqs, 858457221 residues
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| SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Nucleotide sequenc	Nucleotide sequenc	Nucleotide sequenc	Nucleotide segmenc	Nucleotide sequenc	Nucleotide segment	Human ABC1 genomic	Partial human ABC1	Human ABCA1 homolo
SUMMARIES	ID	AAF24680	AAF24702	AAF24685	AAF24686	AAF24707	AAF24708	AAF92831	AAS04035	ABA09200
	DB	22	22	22	22	22	22	22	22	22
	Query Match Length DB ID	10442	10442	10474	10474	10474	10474	183999	446	7086
dР	Query Match	98.0	98.0	98.0	98.0	98.0	98.0	96.4	89.4	89.4
	Score	155.8	155.8	155.8	155.8	155.8	155.8	153.2	142.2	142.2
	Result No.	-	7	က	4	5	9	7	80	6

Human polynucleoti	Human ATP binding	Human ATP binding	Human polynucleoti	Human ABC1 DNA sed	Human ABC1 DNA seq	Human ABC1 gene ex	Human cDNA clone (	CDNA	Human ABC1 cholest	Human ABC1 nucleot	Human ABC1 cDNA.	ABC1	-	-		Human ABC1 cholest		ABC1 polymorphism	Human secreted pro	Nucleotide sequenc	Human ORFX ORF866	Human secreted pro	Human PD-ATP-bindi	Human PD-ATP-bindi	Nucleotide sequenc	Human reproductive	Human secreted pro	Human secreted pro	Human Doc2-beta ge	Human ESRPI protei	Human cDNA encodin	Human polynucleoti	-	Novel protein kina	Human breast and o		
AAK52667	132	AAI70315	AAK51683	AAS06120	AAS06121	AAC69132	AAH07432	AAH18606	AAC69388	AAF83826	AAF92835	AAC69387	AAC69120	AAC69385	AAC69386	AAC69389	AAK70336	AAF93084	AAC06182	AAF25499	AAC75311	AAD05589	AAS08707	AAS08706	AAF54812	AAL07164	AAC01004	AAC01005	AAT79627	ABA08699	AAC66225	AAI59934	AAF77695	AAF44707	AAF21857	PALTONMENTO	ALLGINEENLO
22	22	22	22	22	22	21	22	22	21	22	22	21	21	21	21	21	22	22	21	22	21	22	22	22	22	22	21	21	18	22	21	22	22	22	21		
7086	7260	7260	7281	9741	9854	10545	736	1556	7857	7860	7860	7861	7864	7864	7864	7864	50885	37	298	23024	534	1133	5669	6522	6607	8217	485	532	2043	1093	1727	2143	2644	2668	2853		
89.4	89.4	89.4	89.4	89.4	89.4	89.4	88.4	88.4	85.0	85.0	85.0	85.0	82.0	85.0	85.0	85.0	22.5	22.3	22.0	22.0	21.8	21.8	20.9	20.9	19.7	19.7	19.1	19.1	19.1	19.0	19.0	19.0	19.0	19.0	19.0		
142.2	42.	42.	42.	42.	42.	42.	40.	40.	35.	35.	35.	35.	35.	35.	32.	35.	35.8		35	m		34.6	•				٠.			٠	30.5						
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Human; adenosine triphosphate binding cassette protein 1; ABC1; popolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; haart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                             Nucleotide sequence of a human ABC1 polypeptide.
                                                                                                                                                                              291..7076
/*tag= a
/product= "ABC1 polypeptide"
                                                                                                                                                                     Location/Qualifiers
                   BP
                 AAF24680 standard; DNA; 10442
                                                                                                                                                                                                                                                                               99US-0140264.
99US-0153872.
99US-0166573.
                                                                                                                                                                                                                                                           16-JUN-2000; 2000WO-US16765
                                                          (first entry)
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14-SEP-1999;
19-NOV-1999;
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                                     AAF24680;
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RESULT
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28-DEC-2000
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                                                                                                                                                                                                                                                                                                                                            atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
                                                                                        Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                            The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypetide. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-941. The ABCI genes and proteins are useful for developing pharmaccutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 98.0%; Score 155.8; DB 22; Length 10442; Best Local Similarity 98.7%; Pred. No. 1.7e-36; Matches 157; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
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/product= "ABC1 polypeptide"
                                                                                                                                                                  Disclosure; Page 122-128; 215pp; English.
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291..7076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF24702 standard; DNA; 10442 BP
                                Wade D, Garvin M;
(CVTH-) CV THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2001 (first entry)
                                                           WPI; 2001-137812/14.
                                                                                                                                       atherosclerosis -
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The present sequence encodes a human adenosine triphosphate (ATP)
binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
membranes and utilises ATP hydrolysis to transport a wide variety of
membranes and utilises ATP hydrolysis to transport a wide variety of
ubstrates across the plasma membrane. ABC1 is a pivotal protein in
the apolipoprotein-mediated mobilisation of intracellular cholesterol
stores. ABC1 is defective in Tangier disease, a genetic disorder
characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
localised to chromosome 9422-9431. The ABC1 genes and proteins are
useful for developing pharmaceutical agents for the treatment of heart
disease and other disorders associated with hypercholesterolemia and
atherosclerosis. The genes are useful for developing screening assays to
screen for compounds that regulate the expression of genes associated
with cholesterol transport. The genes and proteins are also useful for
are also useful as diagnostic indicators of cardiovascular disease and
other disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 155.8; DB 22; Length 10442; Pred. No. 1.7e-36; 0; Mismatches 2; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
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                                                                                                                                                                                                                                                                                             Garvin M;
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98.7%;
                                                                                        99US-0153872.
99US-0166573.
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16-JUN-2000; 2000WO-US16591.
                                                                                                                                                                                              (CVIH-) CV THERAPEUTICS INC (UNIW ) UNIV WASHINGTON.
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P-PSDB; AAB31365.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis
                                                                18-JUN-1999;
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Best Local Similarity 98.7%; Pred. No. 1.7e-36;
Matches 157; Conservative 0; Mismatches 2
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99US-0153872.
99US-0166573.
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                   Homo sapiens.
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangler disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangler disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atherosclerosis. The
disorders associated with hypercholesterolemia assays to screen for compounds
the regulate the expression of genes associated with cholesterolemia
transport. The genes and proteins are also useful
as diagnostic indicators of cardiovascular disease and other disorders
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                                                      Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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                   20-APR-2001 (first entry)
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binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangier disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangier disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
9922-9931. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atherosclerosis. The
genes are useful for developing screening assays to screen for compounds
that regulate the expression of genes associated with cholesterol
transport. The genes and proteins are also useful for are also useful
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chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.
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/product= "defective ABC1 polypeptide"
350 ctgctgtggaagaacctcactttcagaagaagacaaaca 388
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DB 22; Length 10474;

Score 155.8; DB 2; Pred. No. 1.7e-36;

98.0%; 98.7%;

Query Match Best Local Similarity

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                                                                                         Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                           1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating a lower than normal high density lipoprotein-cholesterol (MDL-C) lavel, a higher than normal tridlyceride level, or a cardiovascular disease, by administering a compound that modulates or RXR-mediated transcriptional activity
                                                                                                                                                                                                                                                                        98.0%; Score 155.8; DB 22; Length 10474; 98.7%; Pred. No. 1.7e-36; Live 0; Mismatches 2; Indels 0; (
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                             Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
                                                                                                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF92831 standard; DNA; 183999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 1; 317pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayden MR, Brooks-Wilson AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0151977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0526193.
2000US-0213958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000WO-IB01492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ABC1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-244356/25.
                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200115676-A2
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23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYBR-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF92831;
                                                                                                                                                                                                                                                                           Query Match
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53229 ttaatgaccagccacnggcgtccctgctgtgagctctggccgctgccttccagggctccc 53288
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M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the partial coding sequence of human ABC1, which encodes amino acids 1-60 of the human ABC1 protein. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or
                                                                                                                                          9
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Human ABC1 protein, amino acids 1 to 60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, ABC1 gene; atherosclerosis; reverse transport; cholesterol; cardiovascular; neurological; Tangier disease;, LCAT deficiency; lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                              Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
                                                                                                                                        1 ttaatgaccagccacggggttccctgctgtcagctctggccgctgccttccagggctcc
                                                                             22; Length 183999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human ABC1 nucleic acids and polypeptides for treating
                                                                                                                                                                                                                                                                                  53349 ctgctgtggaagaacctcactttcagaagaagacaaaca 53387
triglyceride level, and a cardiovascular disease
                                                                                                                                                                                                                                                                121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                          Score 153.2; DB 2. Pred. No. 2.1e-35;
                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
185..438
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial human ABC1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          AAS04035 standard; cDNA; 446 BP
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                                                                          96.48;
97.58;
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01-MAR-2000; 2000US-0186260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-OCT-2000; 2000WO-EP10886
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AVET ) AVENTIS PHARMA SA.
                                                                          Query Match 96.4
Best Local Similarity 97.5
Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-316327/33.
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Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                       AAS04035;
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; hinbin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; oell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                 also
                                                                                                                                                                                                                                                                                                                                                        152 gagccacacgctgggggggggctgaggggaacatggcttgttggcctcagctgaggttg 211
                                                                                                                                                                                                                                                                              93 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 151
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
               transport of cholesterol. The nucleic acids and polypeptides are all useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                             1 ttaatgaccagccacgggcgtcctgctgtcagctctggccgctgccttccagggctccc
                                                                                                                                                                                                                                                                                                                       gagocacacgctgggcgtgctgggctgagggaacatggcatgttggcctcagctgaggttg
treatment of a disease resulting from dysfunction in the reverse
                                                                                                                                                                                                        7;
                                                                                                                                                                   DB 22; Length 446;
                                                                                                                                                                                                        Indels
                                                                                                             Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.
                                                                                                                                                                 89.4%; Score 142.2; DB 22;
llarity 97.5%; Pred. No. 8.5e-33;
Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                 121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA09200 standard; cDNA; 7086 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2002 (first entry)
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                                                                                                                                                                   Query Match
Best Local Similarity
Matches 155; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABB11956
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contribution also relates to vectors and recombinant noise Comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of detecting the nucleotides or polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into theat probable biological activities, and hence potential therapoutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth activity; have various activity activity; insue growth activity; hemomodulatory activity; tissue growth activity; inmunomodulatory activity; activit or inhibin-related activities; chemotactic or chemotactic or chemokinetic activities; phaemastatic thrombolytic activities; receptor or liquid activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial isofamenta, bone disorders (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial isofamenta, bone disorders (e.g., asthma or arthritis), because in defining them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound cepair (or nucleic acids encoding them) may be used to promote with flower files involved with growth see to encoding the treatment of viral, immunomodulatory activities may be used in the treatment of viral, barterial and fungal inf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a CDNA encoding a
        Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 gagocacacgctgggggtgctggctgagggaacatggcttgttggcctcagctgaggttg 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ttaatgaccaggccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.4%; Score 142.2; DB 22; Length 7086; 97.5%; Pred. No. 1.7e-32; ive 0; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 2196.
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Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to four common polymorphisms in the gene encoding
                                                                                                                   dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 gagccacacgctggggggtgctggctgagggaacatggcttgttggcctcagctgaggttg 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ttaatgaccagccacgggcgtcctgctgtcagctctggccgctgccttccagggctccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                            Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "Human ABC1 protein"
                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2000; 2000EP-0105820
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28-JAN-2002 (first entry)
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Best Local Similarity 97.55
Matches 155; Conservative
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                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI70315
A X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW7832-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 gagccacacgctggggggtgctggctgagggaacatggcttgttggcctcagctgaggttg 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctcc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 142.2; DB 22; Length
Pred. No. 1.7e-32;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 4558-4560; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             were missing at the time of publication.
                                                                                                                                                                                                                                                                   19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-064936.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
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                                                                                                                                                                                                                         2000US-0560875.
2000US-0598075.
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Best Local Similarity 97.5%;
Matches 155; Conservative
                                                                                                                                                     05-FEB-2001; 2001WO-US04098
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                                                        WO200157190-A2.
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
              Homo sapiens.
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Tang YT, Zhao QA,

Xue AJ,

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AAD21326;

AAD21326

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The present sequence is that of CDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter I (ABCI) protein (see AMESO22). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAT70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 N-terminal amino acids to the encoded ABCI protein (see AMESO228). The invention provides 4 common polymorphisms in the ABCI gene. These were identified by sequencing the ABCI gene in different Tangler kindreds. In the variant genes (numbering as in AAT70314), G is changed to A at position 596, T is changed to C at position 1136, A is changed to G at position 596, or any combination of these. All of these polymorphisms alter the amino acid sequence of ABCI and therefore polymorphisms alter the amino acid sequence of ABCI and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G are both associated with a decreased in vitro ApoA-I mediated efflux of cholesterol from mononuclear phagocytes, a feature typical of Tangler disease. 3 of the variants (G596A, A2589G and G3456C) are significantly increased in a population of men having low high density lipoprotein-cholesterol levels and established coronary heart disease (CHD) relative to CHD-free control subjects. The use of the provided ABCI polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular customed and inflammatory diseases (e.g. psoriasis, lupus
                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "alternative open reading frame of AAI70314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                             cholesterol; cardiovascular disease; inflammatory disease;
antiinflammatory; antilipaemic; antipsoriatic; dermatological;
Tangier disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                             ATP binding cassette transporter 1; ABC1; human; lipid disorder;
                                                                         Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 26-28; 41pp; English.
                                                                                                                                                                                                                                                                   Location/Qualifiers 321..7106
                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(2969,G)
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                                     07-JAN-2002 (first entry)
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501..7106
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                                                                                                                                                                                           polymorphism; ss.
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                                                                                                                                                                                                                                 Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                   variation
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AAI70315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ma Y;
                                                                                                                                                                                                             229 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 287
                                                                                                                                                     ttaatgaccagccacgggggtccctgctgtcagctctggccgctgccttccaggggctcc 60
          proteins by antisense or ribozyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Wejhrman T, Goodrich R;
                                                                                              Query Match 89.4%; Score 142.2; DB 22; Length 7260; Best Local Similarity 97.5%; Pred. No. 1.7e-32; Matches 155; Conservative 0; Mismatches 3; Indels 1;
Modulation of ABC1 transcripts or
                                                     Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                      Claim 1; Page 1086-1096; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 228.
                                                                                                                                                                                                                                                                                                                                                                         AAK51683 standard; cDNA; 7281 BP
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27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
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15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
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 erythematodes) is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Yang Y,
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                       AAK51683;
                                                                                                  Query Match
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                               claimed.
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production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                             Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                      gagccacacyctggycytgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brewer HB;
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                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                       ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol; cardiovascular; neurological; Tangier disease;, LCAT deficiency; lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                                           DB 22; Length 7281;
                                                                                                                                                                                                                                                                           1;
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Duverger N, Jaye M, Searfoss GH, Remaley A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                          Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 89.4%; Score 142.2; DB 2. Best Local Similarity 97.5%; Pred. No. 1.7e-32; Matches 155; Conservative 0; Mismatches 3.
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/product= "Human ABC1 protein"
                                                                                                                                                            were missing at the time of publication.
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185..6967
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2000US-0186260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ABC1 DNA sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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01-MAR-2000;
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Lemoine C,
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                                      The sequence represents the coding sequence #1 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other disease e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Naudin L;
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                                                                                                                                                                                                                                                                                                                                                                                                     gagccacacgctgggcgtgctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                    93 ttaatgaccagccac-ggcgtccctgctgtgagctctggccgctgccttccagggctccc 151
                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                                                                                                                                       ttaatgaccagccacggggtccctgctgtcagctctggccgctgccttccagggctccc
                                                                                                                                                                                                                                                                                                                                                                                                                               152 gagccacacgctggggggggctgagggaacatggcttgttggcctcagctgaggttg
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Jaye M, Searfoss GH, Remaley A, B
                                                                                                                                                                                                                              Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
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                                                                                                                                                                                                                                                                          Score 142.2; DB 22;
Pred. No. 1.8e-32;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human ABC1 protein"
              Claim 1; Page 204-208; 368pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
298..7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS06121 standard; cDNA; 9854 BP
                                                                                                                                                                                                                                                                           89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosier-Montus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2000; 2000US-0186260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-EP10886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-0402668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ABC1 DNA sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-316327/33.
P-PSDB; AAU02176.
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200130848-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1999;
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Lemoine C,
                                                                                                                                                                                                                                                                                                        Matches 155;
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                                                                                                                                                                                                                                                                           Query Match
Best Local S
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Db
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New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes -

Claim 1; Page 209-213; 368pp; English.

The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also baseful for treating and preventing acadiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes. 

Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;

Ĥ 1; Gaps Query Match 89.4%; Score 142.2; DB 22; Length 9854; Best Local Similarity 97.5%; Pred. No. 1.8e-32; Matches 155; Conservative 0; Mismatches 3; Indels 1;

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61 gagocacacgotggggggggggggggggggaacatggcatgttggcotcagotgaggttg 120 δ g

121 ò

325

Search completed: September 20, 2002, 03:09:36 Job time: 10645 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 20, 2002, 03:21:58; Search time 110.16 Seconds (without alignments) 354.536 Million cell updates/sec Run on:

US-09-846-456-5 Perfect score:

1 ttaatgaccagccacgggcg......tttcagaagaagacaaaca 159 Sequence:

IDENTITY\_NUC Gapor 1.0 Scoring table:

383533 seqs, 122816752 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 2, Appli	7		i m	,	Sequence 7, Appli	7	Sequence 10, Appl	,			7	Sequence 7, Appli	1	'n	Sequence 1, Appli	4	H	Sequence 1, Appli	7	Sequence 15, Appl	9		2	·	, o	
SUMMARIES	QI .	US-08-866-650-2	US-09-021-287-2	US-09-240-473-2	US-09-144-085-3	US-08-781-802-7	US-08-694-078-7	US-09-058-260-7	US-08-482-073-10	US-07-914-281-7	US-08-393-246-7	US-08-525-058A-7	US-08-696-731-7	US-09-042-531-7	US-08-482-385A-1	US-08-482-385A-5	US-09-422-869-1	US-08-646-981-4	US-08-640-906-1	US-09-395-936-1	US-09-422-869-7	US-09-082-092-15	US-08-911-321-6	US-09-103-840A-1	US-09-010-809-12	US-09-119-788-1	US-08-673-388-9	US-08-614-877-9
	Query Match Length DB	4771 2	4771 2	4771 4	33529 4	3147 2	3147 4	3147 4	2861 4	3647 1	3647 1	3647 1	3647 2	3647 4	1146 1	2728 1	49136 4	318 2	1257 3	1257 4	2001 4	733 4	6176 3	1411529 4	750 3	1633 4	1864 2	1864 2
ďF	Query	18.9	18.9	18.9	18.9	18.5	18.5	18.5	18.0	18.0	18.0	18.0	18.0	18.0	17.6	17.6	17.5	17.4	17.4	17.4	17.4	17.2	17.2	17.2	17.1	17.1	17.1	17.1
	Score	30	30	30	30	29.4	29.4	29.4	28.6	28.6	28.6	28.6	28.6	28.6	28	28	27.8	27.6	7	27.6	27.6	27.4	27.4	27.4	27.2	•	27.2	27.2
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Sequence 29, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 28, Appli Sequence 28, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 20, Appli	
US-08-928-692-29 PCT-US91-00899-4 US-08-530-290-11 US-08-201-200-11 US-09-219-391-11 US-07-841-646-28 US-08-147-023-28 US-08-208-147-023-28 US-08-208-48-7 US-08-408-528A-7 US-08-408-528A-7 US-08-408-528A-7 US-08-40-672-20 US-08-40-7570-28 US-08-40-753A-20 US-08-40-753A-20 US-08-40-753A-20 US-08-40-753A-20 US-08-40-753A-20 US-08-40-753A-20 US-08-40-753A-20 US-08-40-753A-20	
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## ALIGNMENTS

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COTHER INFORMATION: /product= "murine mTll protein"
US-08-866-650-2
                                                                                   APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Takahara, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
VUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: PACE PT PC COMPATIBLE
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                        ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                       Sequence 2, Application US/08866650 Patent No. 5939321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4771 base pairs TYPE: nucleic acid combanneDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 53703
US-08-866-650-2
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Gaps 0 Query Match
18.9%; Score 30; DB 2; Length 4771;
Best Local Similarity 52.4%; Pred. No. 3.2;
Matches 66; Conservative 0; Mismatches 60; Indels

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3 aatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctcccga 62
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Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09240473 Patent No. 6297011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4771 base pairs TYPE: nucleic acid mainfineness; double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.9%;
52.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.9 Best Local Similarity 52.4 Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 611..365
COTHER INFORMATION:
US-09-240-473-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
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                                                                                                     123 gctgtg 128
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                                                                                                                                                                                                                                                                     RESULT 3
US-09-240-473-2
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                                                                                           63 gecacaegetgggegtgetggetgagggaacatggcatgttggcetcagetgaggttget 122
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                                        3 aatgaccagccacggggggtccctgctgtcagctctggccgctgccttccaggggctcccga 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/866,650
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09021287
Patent No. 5981717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.9%;
52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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LENGTH: 4771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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LOCATION: 611..3652
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US-09-021-287-2
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Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Greensp
                                                                                                                                                                                                                                                                                                       123 gctgtg 128
                                                                                                                                                                                                                                                                                                                                                                       261 GCTGAG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-021-287-2
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Sequence 7, Application US/08694078 Patent No. 6218163
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            12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3147 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: mat_peptide
; LOCATION: 245..1231
US-08-781-802-7
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                              GENERAL INFORMATION:
APPLICANT: Gustafsson, Claes
APPLICANT: Gustafsson, Claes
APPLICANT: Ballach, Marry C.
APPLICANT: Julien, Bryan
APPLICANT: Julien, Bryan
APPLICANT: Julien, Bryan
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: 1998-08-31
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: 09/010,809
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE PATENT VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 gecaegggegtectgetgteagetetggeegetgeetteeagggeteeegageeacaeg 70
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APPLICANT: ALLEN, Larry
APPLICANT: ATKENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: VONSTEIN, Veronika
APPLICANT: DEMIRJIAN, David
APPLICANT: DEMIRJIAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.9%; Score 30; DB 4; Length 33529; 54.5%; Pred. No. 5.8; tive 0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 300 S. Wacker Drive 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/781,802
FILING DATE: 10-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 60/019,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                          Sequence 3, Application US/09144085 Patent No. 6280999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08781802
Patent No. 5969121
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-144-085-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.55
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90909
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 33529
US-09-144-085-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-781-802-7
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
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PRILICATION NUMBER: 08 60/001/95

ATTORNEY CROPE WARRENGER: 08 60/001/95

ATTORNEY CROPE WARRENGER: 08 60/001/95

PRESISTANTION NUMBER: 08 60/001/96

PRESISTANTION NUMBER: 08 60/001/
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APPLICANT: Hession, Catherine A.
APPLICANT: Lobb, Roy R.
APPLICANT: Lobb, Roy R.
APPLICANT: Obelon, Susan B.
APPLICANT: Osborn, Laurelee
APPLICANT: Rosa, Margaret D.
TITLE OF INVENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION
TITLE OF INVENTION: ADHESION (MILAS)
APPLICANT: ADHESION (MILAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2798 gootcoccggactacctcccggccggggctttagggctctagtaccaccccatcctg 2857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: cloned esterase OTHER INFORMATION: gene from bacteria E101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29.4; DB 4; Length 3147;
Pred. No. 4.4;
0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2858 gcgtacgccaggatgggggccccggtaaagcctta 2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 goctcagotgaggttgctgctgtggaagaacctca 139
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US 90/02357
FILING DATE: 27-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/452675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1251 Avenue of the Americas
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/827,810
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/486,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-482-073-10/c
; Sequence 10, Application US/08482073
; Patent No. 6307025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%;
56.8%;
                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.8
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY: CDS
, LOCATION: (245)..(1231)
US-09-058-260-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                    LENGTH: 3147
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COUNTRY:
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                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 245..1231
OTHER INFORMATION: /note= "TspA E101 sequence longest
OTHER INFORMATION: open reading frame; other possible start codons are TTG/leu9;
OTHER INFORMATION: TTG/leu13; TTG/leu15; GTG/val43"
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APPLICANT: Allen, Larry
APPLICANT: Allen, Larry
APPLICANT: Allen, Larry
APPLICANT: Allen, Larry
APPLICANT: Alkens, John
APPLICANT: Wonstein, Weronika
APPLICANT: Demirjian, David
APPLICANT: Demirjian, David
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-96-44
CURRENT APPLICATION NUMBER: US/09/058,260B
CURRENT FILING DATE: 1999-04-10
EARLIER APPLICATION NUMBER: 60/001,995
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER FILING DATE: 1996-09-07
EARLIER FILING DATE: 1996-01-11
EARLIER PILING DATE: 1996-01-11
EARLIER FILING DATE: 1996-01-11
EARLIER FILING DATE: 1996-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29.4; DB 4; Length 3147; Pred. No. 4.4; 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2858 GCGTACGCCAGGATGGGGGCCCCGGTAAAGCCTTA 2892
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                  CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
FRICH APPLICATION NUMBER: US 60/009,704
FILING DATE: 10-JAN-1996
FRICH APPLICATION NUMBER: US 60/001,995
FILING DATE: 10-JAN-1995
FRICH APPLICATION NUMBER: 350/001,995
FILING DATE: 10-JAN-1995
FRICHS APPLICATION NUMBER: 37,293
REGISTATION NUMBER: 37,293
REGISTATION NUMBER: 37,293
REGISTATION NUMBER: 37,293
FREERWCE/DOCKET NUMBER: 95,963-C
TELECOMUNICATION INFORMATION:
TELEFAX: 312-913-0001
TELEFAX: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERESTICS:
LENGTH: 3147 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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EARLIER FILING DATE: 1996-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09058260B Patent No. 6218167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.5%;
Best Local Similarity 56.8%;
Matches 54; Conservative (
          07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: mat_peptide
; LOCATION: 245..1231
US-08-694-078-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-058-260-7
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 tgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctcccgagc 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.0%; Score 28.6; DB 4; Length 2861; 57.1%; Pred. No. 7.5; 1ive 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
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NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 CCCAGCCGGCCCACCAGGCCCCGGGAGCT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 cacacgctgggcgtgctggctgagggaacat 95
                                                                                                                                                                                            NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B124CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/359516
FILING DATE: 01-JUN-1989
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APPLICATION NUMBER: US/07/914,281
FILING DATE: 19920720
CLASSIFICATION: 530
                                                                                                                     APPLICATION NUMBER: US 07/354151
FILING DATE: 28-APR-1989
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5324663
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
FILING DATE: 18-DEC-1989
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Best Local Similarity 57.18
Matches 52; Conservative
                                                                                           PRIOR APPLICATION DATA:
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US-08-482-073-10
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ZIP: 22202
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROPIEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Allington
STATE: Virginia
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                                                                                                                                                                                                                                                                  Query Match
18.0%; Score 28.6; DB 1;
Best Local Similarity 57.1%; Pred. No. 8;
Matches 52; Conservative 0; Mismatches 39;
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 30-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAVALLEYE, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REGISTRATION NUMBER: 31,451
RELEPHONE: (703)521-4500
TELEFRAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1673 cccAgccgggccgaggccrcgggaggcT 1643
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APPLICATION NUMBER: US/08/393,24
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08393246
Patent No. 5595900
GENERAL INFORMATION:
                                             LENGTH: 3647 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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ANTI-SENSE: NO

US-08-393-246-7

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; Sequence 7, Application US/09042531
; Patent No. 6268193
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Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                        Arlington
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MOLECULE TYPE:
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    US-08-696-731-7/c
                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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TITLE OF INVENTION: OF OLLGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
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                                                                                                        1733 TGAGCTGGCCAGGACGCCCAACCGGCACCGCCCGTTCTTCTTCCACTGCGCCCGGGG 1674
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
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  Length 3647;
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                                             Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
                                           0; Mismatches 39;
Score 28.6; DB 1;
Pred. No. 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/ACEMT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPER: (703)466-2347
TELER: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08525058A Patent No. 5770420
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    18.0%;
57.1%;
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TYPE: nucleic acid
STRANDEDNESS: double
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                                         52; Conservative
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APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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Matches 52; Conserv
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                      US-08-525-058A-7/c
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                                             Matches
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TITLE OF INVENTION: WETHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 8;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lavalleye, Jean-Paul M. P. REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-UUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 cacacgctgggcgtgctggctgagggaacat
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APPLICATION NUMBER: US/08/696,731
FILING DATE: 14-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/393,246
; Sequence 7, Application US/08696731; Patent No. 5955347; GENERAL INFORMATION: APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ** ARCORMATION.

** TELEKAX: (703)486-234-7

** TELEX: 248855 OPAT UR

** INPORMATION FOR SEQ ID No: 7:

** SEQUENCE CHARACTERISTICS:

** LENGTH: 3647 base pairs

** TYPE: nucleic acid

** STRANDENNESS: unknown

** TOPOIACY
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ilarity 57.1%;
Conservative 0
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  APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

TITLE OF INVENTION: GLYCOLIFIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

CORRESPONDENCE ADDRESS:
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Patent No. 5728561
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
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                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                         STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Aribaton STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,531
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Best Local Similarity 57.1%; Pred. No. 8;
Matches 52; Conservative 0; Mismatches
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APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-UUL-1992
ATTORNEY,AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3647 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0N
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US-09-042-531-7
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Satent No. 5/2002.
GENERAL INFORMATION:
APPLICANT: DEBNOYA,, CLAUDIO D.
TITLE OF INVENTION: GENES ENCODING BRACHED CHAIN ALPHA
TITLE OF INVENTION: KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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17.6%; Score 28; DB 1; Length 1146;
Best Local Similarity 55.0%; Pred. No. 8.7;
Matches 55; Conservative 0; Mismatches 45; Indels
                                                                                        COUNTRY: U.S.A.

ZIP: 10017-5755
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPALIDLE
OPFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,385A
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,385A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHEYKA, ROBERT F.
REGISTRATION NUMBER: 31,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 gcgtgctggctgagggaacatggcatgttggcctcagctg 114
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ADDRESSEE: PETER C. RICHARDSON
STREET: 235 EAST 42ND STREET, 20TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PETER C. RICHARDSON
STREET: 235 EAST 42ND STREET, 20TH FLOOR
CITY: NEW YORK
COUNTRY: US.A
ZIP: 10017-5755
                                                                                                                                                                                                                                                                                                                                                                                                                                     PC8346C
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/08482385A; Patent No. 5728561
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: SHEKKA, ROBERT F.
REGISTRATION NUMBER: 31,304
REFERENCE/DOCKET NUMBER: PC83.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-573-1189
TELEPHONE: 212-573-1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-573-1939 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1146 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                      NEW YORK
                                             CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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US-08-482-385A-5/c
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REFERENCE/DOCKET NUMBER: PC8346C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-573-189
TELEFAX: 212-573-189
TELEFAX: 212-573-189
TELEFAX: 212-573-189
SEQUENCE CHARACTERISTICS:
LENGTH: 2728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-482-385A-5
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ô Query Match 17.6%; Score 28; DB 1; Length 2728; Best Local Similarity 55.0%; Pred. No. 11; Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps

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Search completed: September 20, 2002, 03:22:05 Job time: 14214 sec

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September 20, 2002, 01:23:18; Search time 3895 Seconds (without alignments) 550.967 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                   OM nucleic - nucleic search, using sw model
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159
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                                                                                                                                                                                                                Sequence:
                                                                                                          Run on:
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Databas

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

EST: em_estba:* em_esthum:* em_estin:* em_estov:* em_estov:* em_estro:* em_estro:* em_htc:* gb_est!:*	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	21125500 ATT25500	DOCCCTOW DOCCCTOW	BB657864 BB657864	Z44377 HSC1ZB081 n	BG384217 303216 MA	AA914462 vz01f08.r	AV845237 AV845237	BH087817 RPCI-24-3	AQ848626 LMAJFV1_1	AV862022 AV862022	AW751638 RC5-CT007	BB843149 BB843149	BF484412 WHE2323_B	BE471178 WHE0285_G	BM149133 TCAAP2E63	BG325753 602424464	AV864011 AV864011	AV892280 AV892280	
•	ID	11111111111111111111111111111111111111	AUISOSEB	BB657864	244377	BG384217	AA914462	AV845237	BH087817		AV862022	AW751638	BB843149	BF484412	BE471178	BM149133	BG325753	AV864011	AV892280	
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æ	Query Match		88.4	45.8	44.5	44.5	23.3	22.6	22.4	22.3	22.0	21.9	21.9	21.9	21.9	21.8	21.8	21.6	21.6	
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BH087727 BG398045 AW313960 AQ885360 BI541694		BBABB	m &	12 AQ452008 10 BE981503 9 BB644307 10 BE981359 12 AQ745776 9 AA726802
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## ALIGNMENTS

AU135588 736 bp mRNA linear EST 24-OCT-2000 AU135588 PLACEI Homo sapiens cDNA clone PLACE1002437 5', mRNA sequence. AU135588 AU135588 I GI:10996127 EST.  Houns sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Elekarnatis, Prinates Catarrhin; Homio.	Mandalia ja Lullalia, Filmaces, Cataliania, Calabases 1 to 736) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T., HRI human cDNA project Unpublished (2000) Genomics Laboratory Helix Research Institute 15313 Yana, Kisarazu, Chiba 292-0812, Japan Fat: 81-438-52-3951 Fax: 81-438-52-3951	& 3'-end one pas orary constructic cal Science, Univ s oiens" 37" anta" 185FL3"	ัช
AU13588 AU13588 PLACE1 Homes sequence. AU135588.1 GI:1099 EST. human. Homo sapiens	manufalia; bulleriad, 1 (bases 1 to 736) Ota,T., Nishikawa,T. Yamamoto,J., Wakama,T. Sogai,T. HRI human cDNA proj(Gnoublished (2000) Contact: Research Inst 1532-3 Yamanushan, Sasara 1438-52-3952 Pars, 181-438-52-3952	Emall: genom: HRI human cDI Research Inst Virology, Inst Helix Research 1.  / Org / Ab	
RESULT 1 AU135588 LOCCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	BASE COUNT ORIGIN

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                                 FEATURES
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Arakwa'T. Carninci, Pittuda'S., Furuno, M., Hanagaki, T., Hara, A.
Arakwa'T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kwai, J., Konno, H., Kouda
,M., Koya, S., Matsuyama'T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Takeda, Y., Soyabe, Y., Suzuki, H.,
Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Conno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa, K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh
Carninci.p., Shibata.Y., Hayatsu.N., and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
Prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fuliwake.S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E.,
Watahiki.M., Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka,T., Matsu.r.,
.S., Kawai.J., Okazaki.Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshings, Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB657864 BIKEN full-length enriched, 12 days embryo eyeball Mus
musculus cDNA clone D230019D04 5', mRNA sequence.
                                                                                                                                                                                                                                                            122 TTATION TO THE TOTAL TO THE
                                                                                                                                                                                                                                                                                                                                                                            61 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 GAGCCACACGCTGGGGTGCTGACGGAACATGGCTTGTTGGCCCCAGCTGAGGTTG 340
                                                                                                                    Gaps
                                                                                                                                                                                        1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RİKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                    1;
                        DB 9; Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                    Indels
                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 CTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACA 379
    88.4%; Score 140.6; DB 9 96.9%; Pred. No. 1.4e-28; Live 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB657864.1 GI:16491690
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                                                                                                 Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki,Y.
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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BB657864
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TITLE COMMENT

SOURCE

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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                           /db_xref="taxon:10090"
/clone="D230019D04"
/clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sebastiani-Kabaktchis,C. and Tessier,A. IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 TTAATGACCAGCCAC-AGAGTCACAGCTCTGTGCTGGCTGCT-CCCTCCAGGGCTCTC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 gagccaca-----cgctgggggtgctgagggaacatggcatgttggcctcag 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSC1ZB081 normalized infant brain cDNA Homo sapiens cDNA clone c-1zb08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 GAGCCGCAGACGCAGGTCGCTGTGGGTGCCGGCTGTGGTGACATGGCTTGTTGGCCTCAG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genethon Centre de recherche sur le Genome Humain
1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
45.8%; Score 72.8; DB 9; Length 619;
Best Local Similarity 77.4%; Pred. No. 5.9e-10;
Matches 130; Conservative 0; Mismatches 27; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995) 95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 ctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRNA
                                                                                                                                                                          /dev_stage="12 days embryo"
/lab_host="DH10B"
                                         /organism="Mus musculus"
                                                                                                                                                     /tissue_type="eyeball"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 bp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z44377.1 GI:573506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and its expression
                                                                                                                              eyeball"
                       .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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/tissue_type="total brain"
/dev.stage="3 months old"
/dev.stage="3 months old"
/note="corgan: brain, Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev.stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primad and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Cetartiodactyla, Suina; Suidae, Sus.
1 (bases 1 to 535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 TTAATGANCAGCCAC-GGCGTCCCTGCTGAGCTCTGGCCGCTGCCTTCCAGGGNTCCC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ttaatgaccagccacgggcgtccctgctgtcagctctggccgctgccttccagggctccc 60
                                                               Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1zb08
Seq primer: (-21)M13_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.5%; Score 70.8; DB 10; Length 292; 94.3%; Pred. No. 1.7e-09; Live 0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ысындыү
303216 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG384217
                                                                                                                                                                                                                                          /clone_lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4360 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTACAGGACG
Plate: 90 row: G column: 13
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="c-1zb08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genexpress@genethon.fr
Single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.39
Matches 83; Conservative
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRimers
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                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG384217
                                                                                                                       FEATURES
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AA914462 440 bp mRNA linear EST 14-APR-1998 vz01f08.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1314471 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Lacy,M., La,M., Martin,J., Morris,M., Schellenberg,K., Sreptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                           /clone_lib="MARC lpIG"
/tissue_type="pooled"
/lab host="Nath10B"
/note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                 54 ggctcccgagccacacgctgggcgtgctgagggaacatggcatgttggcctcagct 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 GGAGCCACACGCAGGCTGGTGTGTGTGCCAGCTGAGGTAACATGGCTTATTGGACTCAACT 303
                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                  Length 535;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 gaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 GAGGTTACTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xr=aron:10090"
/clone="IMAGE:1314471"
/clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                             Score 70.8; DB 10;
Pred. No. 2e-09;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 439.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
/organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA914462.1 GI:3053854
                                                                                                                                                                                                                                                                                                ch 44.5%; ll Similarity 79.2%; 84; Conservative (
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Best Local Similarity
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AQ848626.1 GI:6053274
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60.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: BAC ends
                                                                                                      DNA sequence.
                                                                                                                                                                                            Mus musculus
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Best Local Sima
'-- 59;
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T 3']; double-stranded cDNA was ligated to Eco RI addeptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pf7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
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Eukaryota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia: Cionidae; Ciona.
1 (bases 1 to 533)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="rcieg08c18"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 ccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 ATGGAGAGCCAAAGATCTGCATGTTCTGTACACTGAACTCTGCTTTCATTGGATCAAAAT 127
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ccctgctgtcagctctggccgctgccttccagggctcccgagccacacgctgggcgtgct 81
                                                                                                                                                                                                                                                                         148 CGCTGCGGTCAAGGCCTCCCGCTCTCTCCCAGTGCTTCCCCGCCGTGCCAGGCCCTTGCG 89
                                                                                                                                                                                                                                                                                                           82 ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctc 138
                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                          AV845237 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone rcieg08c18 3', mRNA sequence.
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                                                                                                                                                                     Score 37; DB 9; Length 440;
Pred. No. 3.8;
0; Mismatches 50; Indels
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                                                                                                      1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: satoh@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ciona intestinalis"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ctgtggaagaacctcactttcagaagaagacaaaca 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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113 c 94
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                                                                                                                                                                        23.3%; 57.3%;
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Matches 67; Conservative
                                                                                      Bonaldo.
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Best Local Similarity
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Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejongémail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 382 row: O column: 9
Seq primer: SP6
BH087817 514 bp DNA linear GSS 18-JUL-2001
RPCI-24-38209, TJ RPCI-24 Mus musculus genomic clone RPCI-24-38209,
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Mouse BAC End Sequences from Library RPCI-24
Contact: Shaying Zao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ848626 LMAJFV1_lm12d06.x1 Leishmania major FV1 random genomic library Leishmania major ell mAJFV1_lm12d06 3', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 AACCATTCTCTGTGCGTCTCTGATAGCAAAGGAAAGCTCAAGAGCTTAAGATGTGGTTTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.6; DB
Pred. No. 9.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="RPCI-24-38209"
/clone_lib="RPCI-24"
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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/clone="rcieg31005"
/clone=lib="Nori Satch unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
/ 116 c 99 g 201 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttgctg 123
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                                                                                                                                                  1 (bases 1 to 571)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                    Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Ciona intestinalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                        AV862022.1 GI:16849546
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Mammalia; Eutheria;
1 (bases 1 to 301)
                                                                 Ciona intestinalis.
                                                                                          Ciona intestinalis
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N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing' and the Washington University Genome Expending Center For information on obtaining clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. Seq primer: -400P from Gibco
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                                                                                                                         Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blastain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by
                                                                                                                                                                                                                                                                              shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="LMAJFV1_im12d06"
/clone_lib="Leishmania major FV1 random genomic library"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                        Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
                                                                                                                                                                                                                                                                                                                      Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
                                                                                                                                                                                                                                                                                                                                                          Other GSSs: lm12d06.yl
Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
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57.8%;
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Fax: 314 286 1810
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AW751638 301 bp mRNA linear EST 28-APR-2000 RC5-CT0071-041099-002-g07 CT0071 Homo sapiens cDNA, mRNA sequence. AW751638
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                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                        Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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1 (bases 1 to 516)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone="F43009P04"
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Contact: Olin Anderson
     1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawai, J., Kolina, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okayaki, Sahito, K., Sahata, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB843149 365 bp mRNA linear EST 26-NOV-2001 BB843149 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430009P04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: colon; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ...)716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-CT0071-041099-002-g07&t3=1999-10-04&t4=1)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 tgctggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacct 137
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53.7%; Pred. No. 14;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0071"
/dev_stage="Adult"
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70 c 85 a
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High quality sequence stop: 64.
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                                        Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Wheat pre-anthesis spike cDNA library"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_l: EcoRI; Site_l: XhOI; Plants were grown in the
greenhouse. Whole Spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a CDNA library was made, and
the CDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
US Department of Agriculture, Agriculture Research Service, Pacific
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US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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                                                                                                                                                                                                                    Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.

Location/Qualifiers
1. 516
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Pred. No. 16;
0; Mismatches 47; Indels 0;
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                                      West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
TTE1: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2323_B07_D13"
                                                                                                                                                                                         Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: oandersn@pw.usda.gov
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il Similarity 57.3%;
63; Conservative
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1...530
/organism="Trititum aestivum"
/cultivar="Chinese Spring"
/db_xref="kason:4565"
/clone="Webcor.4565"
/clone=lib="Wheat drought-stressed seedling cDNA library"
/tissue_type="Seedling without endosperm"
/dev.stage="Five day old seedling"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni ZAP XR, excised phagemid;
/note="Vector: Lambda Uni ZAP XR, excised phagemid;
/site=1: ECORI; Site=2: XhoI; Seeds were surface-sterilized
/germinated and grown aseptically in the dark at room
temperature on filter paper with water, nysterin and
cefotaxime in covered crystallization dishes. Five-day old
seedlings were incubated for one day at 90% RR. After
removing endosperm, seedlings were transferred to
desiccator jar containing saturated MgSO4 at room
temperature for 24 hr. The tissue, total RNA, and poly(A)
RNA were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 344)
Wei,Y., Tsang,Y.T.M. Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 CGCCGCTGCCGACATCTCCGACCCATGACGAGCAGCTCAGTCAAGACAGATGTGCGGCAG 334
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Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratgene SK primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 gctggctgagggaacatggcatgttggcctcagctgaggttgctgctgtg 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 GGGAGAAAAGGAAGATTGGGATGCCGGCATCATCTCTGGACGCCGCTGTG 384
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1102 Bates, MC3-3320 Houston, TX 77030, USA
171: 832-824-4536
Fax: 832-825-4038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM149133.1 GI:17170474
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Best Local Similarity
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                                                                                                                                                                                                                                                         /note="Vector: lambda pSB; Site_1: BamHI; Site_2: ECORI; First strand cDNA was primed with an anchored Xhol-oligo(dT) primer [5'GGAGGACTGGGGGGCGCGCGGGGGGGGGGGGT)VN 3'; V-A,C,G; N-A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer [5'AGAGACTCGGACCCCATAATAATAATAATC] 3']. Jand then digested with BamHI and Xhol bouble-stranded cDNA was then digested with BamHI and Xhol and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P. Westover A. Nishiyama Y., Okbumi T., Itoh M. Nagaoka S. SasakiN. Okazaki Y. Muramatsu M. Schneider C. Hayashizaki Y. High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
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602424464F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4562559 5',
                                                                           /clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project=TCAA"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1574)
1 (bases 1 to 1574)
1 Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML274 row: p column: 16
High quality sequence start: 5
High quality sequence stop: 178.
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                                                                                                                                                             /tissue_type="leukopheresis"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                     /clone="TCAAP6391"
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                                                                                                                                   /sex="male"
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BG325753
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.8%; Score 34.6; DB 10; Length 1574; 55.4%; Pred. No. 25; vative 0; Mismatches 54; Indels 0;
/db_xref="taxon:9606"
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Best Local Similarity
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AC107969 HOMO SAPI
AL023575 HUMBAN DNA
AC107939 HOMO SAPI
AC013494 HOMO SAPI
AC013495 HOMO SAPI
AC018988 HOMO SAPI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Rosier-Montus,M.F., Remaley,A. and Santamarina-Fojo,S.
Repulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NOV-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Sequence 1 from Patent WOO183746.
AX351029
AX351029.1 GI:18616385
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/organism="Homo sapiens"
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AUTHORS
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VERSION
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(without alignments)
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1797656 seqs, 10463268293 residues
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Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P.,
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 3 08-NoV-2001;
Aventis Pharma S.A. (FR)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 3 from Patent W00183746.
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Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1)
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Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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33331. 181457
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33931. 34151
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                                                Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse abcal comparative sequencing and transgenesis studies revealing novel regulatory sequences Genomics 73 (1), 66-76 (2001)
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission

    201144
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    /db_xref="taxon:9606"

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78931. .79049 /gene="ABCA1"

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/number=3 77520. .77661 /gene="ABCA1"

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SWSDMRQEVMFLINVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
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HHDEADVLOCABLAILSHGKACCVGSSELEKROLGGTGTYTLTVKKDVSESLSSCRNSS
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LQPWMYNEQYTFVSNDAAPEDTGTLELLNALTKDPGFGTRCMGGNPIPDTPCQAGEEW
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DILQDLFGRNISDYLVKTYVQI IAKSLKNK IWVNEFRYGGFSLGVSNTQALPPSQEVN
DAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
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PASFVVELIODENSKKHLOPISGVERVFVIWLGENVVVAPATVITIFCFQO
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 149034)

Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genomic sequence of the human ABCA1 gene: analysis of the
                                                                                                                                                                                                                  32389 TCCAGAATTCCTTGCCTGGTGGCCTCCACATGCACTTCCAGGGCCTGCTTGGGCCTCTTC 32448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32149 AACAGGCGCCCGCCACCATCTGGCTAATTTTTGTATTTTAGTAAAGACTGGGTTTCA 32208
                                                                        tccagaattccttgcctggtggcctccacatgcacttccagggcctgcttgggcctcttc 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois, T.L. and Brewer, H.B. Jr.
                                                                                                                                                                                                                                                                                                                                                                       agggcaaacagtccatggtgcaaaggggccatgccacccagagttatgagtacctgggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggtggtgggagttctggaatatgatggagctggaggtgggaagagagtaggcttgggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse ATP-binding cassette A promoter
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Homo sapiens ABCA1 (ABCA1) gene, complete cds.
AF275948
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AUTHORS
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AF275948
LOCUS
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KEYWORDS

SOURCE

TITLE

TITLE

VERSION

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KLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT
NKIKDSYMDPGPRADPFEDNRYWGGFAYLODVVEGAIIRVLTGTEKKTGVYWQOMPY
PCYVDDIFLRVWSRSMPLFWTLAMIYSVAVIIKGIVEKERRIKETMRIMGLDNSILW
FSWFISSLIPLLVSAGLLVVILKGNLLPYSDPSVVRPLSYPRAVTILOFELISTLE
SRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAXLLSPVAFGFGCEYFALFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGWTWYIEAVFPGQYGIPRPW
YFPCTKSYRFGEESDEKSHFGSNQKRISEIOMEEEPTHLKLGVSIQNLYKVYRDGMKV
YODGLALDHYFEGQITSFLEMGAGKTTYMSILTGLEFPTSGTAYILGKDIRSEMSTIK
QNLGVCPQHWVLFDNLTYEBIIWFYARLKGISEKHVRAEMEQMALDYGLPSSKLKSKT
SQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQGRTIILST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETS
DGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
GWKLTQQQFVALLWRRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQPWWYNEQYTFVSNDAPEDTGTLELLNA<sup>†</sup>IKDPGFGTRCMEGNPIPDTPCQAGEEEW
TATAVPQTIMDLEQNGNWANNSPACCSSNSIKTKALLVEVPERAGGEEDPQRKGNTA
DILQDLTGRNISDLYVTYQJIAKSEKNK TWVNEFRYGGFSLGVSWTQALPPSGEVN
DAXKQMKKHLKLAKDSSADRFLNSLGRFWTGLDTRNNVFWFNNKGWHAISSFLNVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAXMTTSVDVLVSICVIFAMSFV
PASFVVFLIQERVSKAKHLQFISGVKPVIYMLSNFVMDMCNYVVPATLVIIFICFQQ
KSYVSSTNLPVLALLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLSSCRNSS
STVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVS
PLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTGDTTVTRCDAFLNXNSILSNIHEVHQNMGYCPQFDAITELLIGREHVEFFALLRGV
PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
                                                                                                                                                                             NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
                                                                                                                                                                                                                 REKLAAAERVLRSNMDILKPILRTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMR
                                                                                                                                                                                                                                             SWSDMRQEVMFLINVNSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
                                                                                                                                                                                                                                                                                                                RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE
                                                                                                                                                                                                                                                                                                                                                    <u>QOLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RILDGGGQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKM
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVXKEKHRNMLQYQLPSSLSSLARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT
                                                                      /translation="MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRL
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/rpt_family="Alu"
38995. 3077
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37999. .38166
/rpt_family="Alu"
38172. .38269
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44349. .44626
/rpt_family="Alu"
48473. .48669
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36167. .36440
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31050. .31314
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31692. .31973
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37617. .37892
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41547. .41565
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41657. .41679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFLQDEKVKESYV"
29916. .30180
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aattttacacgactgcaattctctggctgcacttcacaaatgtatacaaactaaatacaa 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agctctctcatgccacctcattctggccaaaactcaggtcaaactgtgaagagtctaaat 1624
                                                                                                                                                                                                                                                                                                                                                       GGTGGTGGGAGTTCTGGAATATGATGGAGCTGGAGGTGGGAAGAGAAGTAGGCTTGGGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AGCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 149034;
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                                                                                                                                                                                                                                                                                                                         Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                  46.0%; Score 1487;
                                                                                     55297, .55344
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58501, .58935
/note="LTR"
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62812. .63077
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69481. .69760
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55029. :55226
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55297. :55344
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50547. .50614
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54285. .54418
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68499. .68731
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67123. .67382
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                                                                                                                                                                                                                                                                                             /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                          99.88;
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Direct Submission

Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Independent CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Jan 15, 2002 this sequence version replaced gi:18121468

During sequence assembly data is comparated from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality)=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em; EMBL; Sw;;

SWISSPROT; Tr;, TREMBL; Wp;, WORNPEP; Information on the WORNPEP

database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping

droup. A. Marcharian and the sanger can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                               PRI 11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                               96717 bp DNA linear PRI 11-JAN-2005 sequence from clone RP11-217B7 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chr9
RP11-217B7 is from the library RPCI-11.1 constructed by the group
Of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Sequence from AF275948 sequenced by National
Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
                                                                                                                                /organism="Homo sapiens"
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3238. .3278
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/note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
/note="Sequence from overlapping clone RP11-122F10 (AC026643). Assembly confirmed by restriction digest." 92050. 92163 /note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                      19014 AAAGACTGGGTTTCATCATGTTGGCCAGGTTGGTTTCGAACTCCTGACCTGAGGTGAGCT 18955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18714 TGGCCTTGAGCCGTGGCCTGGAGATCCTGTTGACTGTAGCATGGAGGGGGCTTGTGCAGC 18655
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    18654 TGAATGTCTGTATGCAGGTGGTGGGAGTTCTGGAATATGATGAGGGCTGGAGGTGGGAAGA 18595
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Hayden, M. N., Brooks-Wilson, A. R., Pimstone, S. N. and Clee, S. M.
Hayden, M. M., Brooks-Wilson, A. R., Pimstone, S. N. and Clee, S. M.
Compositions and methods for modulating hdl cholesterol and
triglyceride levels
Patent: WO 0115676-A 1 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              782 atgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaagtttgac 841
                             gaagtaggcttggggcagctctctcatgccacctcattctggccaaaactcaggtcaaac
                                                        18594 GAAGTAGGCTTGGGGCAGCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAAC
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37944 c 41170 g 54950
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/organism="Homo sapiens"
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Sequence 1 from Patent W00115676.
AX092589
                                                                                                                                                                                                                          18414 TCTGTCCTGAGTCTTCTATGAATC 18391
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HTG 22-APR-2000
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens, clone RP11-1M10
27331 IGGCCIGGAGATCCTGTIGACTGTAGCATGAGGGGGTTTTIGITITITITIT 11 27390
                                                                                                                                                                                                                                                                                            1202 teccaaagtgetgggattacaggeatgagecactgegeecageteagatecatecette 1261
                                                                          1262 taagggcaaacagtccatggtgcaaaggggccatgccacccagagttatgagtacctggg 1321
                                                                                                                                                                                                       1442 tggcctggagatcctgttgactgtagcatggagggggcttgtgcagctgaatgtctgcat 1501
                                                                                    1382 tctatgcgtctgtcctgagtgttgatagaaccactgatgtgagtacctgggcttgagccg
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AC012230.3 GI:7637254
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Submitted (21-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 22, 2000 this sequence version replaced gi:6454033. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                 Center project name: L2310

Center clone name: L_M 10

Center clone name: L_M 10

Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 117571 bases at least Q40

Consensus quality: 145749 bases at least Q20

Insert size: 185000; agarose-fp

Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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1994 bp in length
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contig of 1707 bp in length
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12354 15228: contig of 2875 bp in length
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22587: contig of 2356 bp in length
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contig of 2377 bp in length
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38318: con+
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1104 2634: cont
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2735 4415: cont
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9686: con
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45449 45548: gap of

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117308 117407: gap of 100 bp 117408 124080 124179: gap of 100 bp 124080 124179: gap of 100 bp 124189 131281: contig of 6672 bp in length 131282 131381: gap of 100 bp 131382 13181: gap of 100 bp 131382 138159: gap of 100 bp 131860 138159: gap of 100 bp 131860 145491: contig of 7332 bp in length 145492 145591: gap of 100 bp 145592 157391: contig of 13800 bp in length 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 100 bp 157392 157491: gap of 17573 bp in length.
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320: gap of 100 bp
93499: contig
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F 5015 bp in length
                48216: gap of 100 bp 52618: contig of 4402 bp in length 52718: gap of 100 bp 5592: contig of 3874 bp in length
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contig of 2943 bp in length
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82113: contig of 5125 bp in length
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48116: contig of 2568 bp in length
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88220: con
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 167)

Porsch-Ozcurumez, M., Langmann, T., Heimerl, S., Borsukova, H., Kaminski, W.E., Drobnik, W., Honer, C., Schumacher, C. and Schmitz, G. The zinc finger protein 202 (znf202) is a transcriptional repressor of atp binding cassette transporter al (abcal) and abcgl gene expression and a modulator of cellular lipid efflux

J. Blod. Chem. 276 (15), 12427-12433 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgttttgtttcgaggccaaggaggttcgggaagtgctcggtttcggggactttgatccg 3209
3558 GGGAACGGGGGGGGGGGGGGGAGGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCG 3617
                                                                                                                           3798 TITCCCCGGTICTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAG 3857
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Homo sapiens partial ABC-1 gene for ATP-binding cassette
transporter-1, 5'UTR and promoter region.
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1. .1167
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1. .1167
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1167)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,

Analysis of hABCI gene 5' end: additional peptide sequence,

Analysis of hABCI gene 5' end: additional peptide sequence,

promoter region, and four polymorphisms

Hes. Commun. 271 (2000) In press

2 (bases 224 to 1167)

RS Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,

Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene,
promoter and exon 1.
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Submitted (20-ARR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
3 (bases 1 to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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Submitted (23-JUN-2000) Cardiovascular Research Institute,
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On Jun 23, 2000 this sequence version replaced gi:7769713.
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/db_xref="taxon:9606"
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/gene="ABCA1"
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PAT 22-JAN-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
                                                                                                                      2489
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                                                         942
                                                                                                                                      647
                                                                                                                                                                                                                                                                                                                                     648 GAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCAC----CCCCACC 702
                            348 CCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCCTTTGAAAGGAAAC 407
ccattacccagaggactgtccgccttcccctcaccccagcctaggcctttgaaaggaaac
                                                                                                                         GCGCCCAGCCCCAGCCCAGCGCTTCCCGCGCGTCTTAGGCCGGGGGCCCGGGGGG
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AUTHORS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1643)

Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.

Atp binding cassette transporter protein abcl polypeptides

Patent: WO 0078971-A 3 28-DEC-2000;

CV THERAPEUTICS, INC. (US)

        2610
        gaaggggaccgcgggaccctaagacacctgctgtaccctccaccccaccccacc
        2669

        1274
        GAAGGGGACGCAGACCCTAAGACACCTGCTGTACCCTCCACCCCACCCCACC
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                                                                                                           Length 1643;
                                                                                                                    Pred. No. 3.9e-302;
                                                                                                         16.7%; Score 541; DB 6;
100.0%; Pred. No. 3.9e-302
tive 0; Mismatches 0;
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Patent: WO 0078972-A 3 28-DEC-2000;
                                                               403
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Sequence 3 from Patent WO0078971.
                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
413 c 457 g 40
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Location/Qualifiers
          VEUTICS, INC. (US)
Location/Qualifiers
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           CV THERAPEUTICS, INC.
                                                                                                                                Matches 541; Conservative
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Birran, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Bodspel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69570)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-1N10
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                                                                                                                                                                                                                                                                                                                                                                                               1094 CCAATCCCTCCGTCAGAAACTAACAAAGAAAAAAAAATTGCGAAAGCAGA 1153
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                                                                                                                                                                             2370 aaaagacaagacaaaatgattggcgtcctgagggagattcagcctagagctctctccc
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Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
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0
                                                                                                       Length 1643;
                                                                                                                                           0; Indels
                                                                                                         16.7%; Score 541; DB 6; L4 100.0%; Pred. No. 3.9e-302; iive 0; Mismatches 0;
                                     403
/organism="Homo sapiens"
/db_xref="taxon:9606"
413 c 457 g 403
                                   457 g
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Matches 541; Conservative
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              Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Merwan, P., McGrnan, K., McChaeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisan, I.C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission
                                                                                                                                                                                                                                 Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 0. Jul 13, 2000 this sequence version replaced g1:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This record contains 73 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Wordtact: sequence_submissions@genome.wi.mit.edu
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contig of 851 bp in length
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14241: contig of 861 bp in length
100 bp
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contig of 869 bp in length
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100 bp
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10376: contig of 846 bp in length
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Center clone name: 1_N_10
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13280: cont
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6540: con
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2468: gap of 100 bp 3312: contig of 844 bp in length 3412: gap of 100 bp 34268: contig of 856 bp in length 4368: gap of 100 bp 35204: contig of 836 bp in length 5364: gap of 100 bp 35204: contig of 852 bp in length 36156: contig of 852 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
1855 bp in length
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1872 bp in length
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f 834 bp in length
                                                                                                                                                                                           80: gap of 100 bp 24733: contig of 853 bp in length 33: gap of 100 bp 105709: contig of 837 bp in length 70: gap of 100 bp 26621: contig of 851 bp in length
                                                                                                                                                                                                                                                                                                      p of 100 bp contig of 856 bp in length p of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35: gap of 2040: contig of 855 bp in lengum. 40: gap of 100 bp 51404: contig of 864 bp in length
                 in length
                                          in length
                                                                       in length
                                                                                                 in length
                                                                                                                                                                                                                                                                            21: gap of 100 bp
27576: contig of 855 bp in length
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                                                                               0066: gap of 100 bp 20921: contig of 855 bp in 21865: contig of 844 bp in 965: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 39131; gap of 100 bp

2 40006; contig of 875 bp ir

7 40166; gap of 100 bp

4 41913; contig of 861 bp ir

8 41067; gap of 100 bp

8 41913; contig of 846 bp ir
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                          18141: gap of 100 bp
19009: contig of 868 bp
19109: gap of 100 bp
19966: contig of 857 bp
17172: gap of 100 bp
18041: contig of 869 bp
18141: gap of 100 bp
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46643: contig of 819 bp
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49485: contig of 834
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43776: contig of
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v: gap of
28532:
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32368:
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31410: cont
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33312: con
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36156: cont
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9686: contig of
9786: gap of 10
                                     AC012230.3 GI:7637254
HTG; HTGS_PHASE1; HTGS_DRAFT
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1104 2634: cor
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4516 5785; cor
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5886 7879; cor
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                                                                                                                                                                             ORGANISM
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ACCESSION
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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63827: contig of 861 bp in length
63927: gap of 100 bp
64783: contig of 856 bp in length
64883: gap of 100 bp
65740: contig of 857 bp in length
                                     52373 52472: gap of 100 bp

52473 53328: contig of 856 bp in length

53429 54268: contig of 840 bp in length

54269 54368: gap of 100 bp
                                                                                                                                                                                                                                                                                                            56197: contig of 868 bp in length
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29: gap of 100 bp
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57163: contig of 866 bp in length
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contig of 868 bp
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55330 56199
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qq δŽ g ŏ g Qγ

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14574 bases at least Q40
Consensus quality: 145749 bases at least Q20
Consensus quality: 160940 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L2510
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12253: contig of 2467 bp in length 53: gap of 100 bp
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45448: contig of 2513 bp in length
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert construction, 5'- 6 3'-end one pass sequencing and clone selection: Helix Research Association for Biotechnology; cDNA library construction, 5'- 6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

Location/Qualifiers
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2 (bases 1 to 1750)

Isogai, T., and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
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                      1405 TGCCAAGGAGCTCAAAGGTTTCAACAAAGTTCACTTTCAGAAAACCCCTTTGAGGAAGAC 1346
                                                                                          61 GGGTGCGGCAGGGCAGGGCGGGAGCTCCGCGCACAACAGAGCCGGTTCTCAGGGCGC 120
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oligo capping; fis (full insert sequence).
Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMAl
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100.0%; Pred. No. 4.6e-183;
tive 0; Mismatches 0;
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/translation="wacwpolrllimknifferrotolllevawplfifillsvrl
SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKS"
198 c 190 q 156 t 1 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABC1 gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 697)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Direct Submission
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/protein_id="AAF69513.1"
/db_xref="G1:7769708"
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100.0%; Pred. No. 6.1e-164;
tive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bederly, R., Beda, F., Lanton, L., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Domino, M., Doyle, M., Cooke, P., Galagan, J., FitzHugh, W., Porrest, C., Gage, D., Galagan, J., Reratas, P., FitzHugh, W., Porrest, C., Gage, D., Galagan, J., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Lieu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Marquis, N., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Plerre, C., Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Lyar, T. M., Peterson, K., Plerre, N., Pisland, C., Pollara, V., Raymond, C., Rilley, R., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wuyman, D., Ye, W.J., Zimmer, A. and Zody, M., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Wassiliev, H., Viel, R., Vo, A., Wuyman, D., Ye, W.J., Direct, Subnission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
             ccttctccggaaggcttgtcaagggtaggagaagaagacgcaaacacaaaagtggaaa 3111
                                                                                                   caacagagccggttctcagggcgctttgctccttgtttttccccggttctgttttctcc 3051
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                                                       241 CCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAGAGACGCAAACACAAAAAGTGGAAAA 300
                                                                                                                    ACC21345 90698 bp DNA linear HTG 1
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
ACC21345
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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is updated, the accession number will
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Schmitz, G. and Bodzioch, M.
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                      8.7%; Score 282; DB 2; L ilarity 99.7%; Pred. No. 1.6e-151; Conservative 0; Mismatches 1;
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/db_xref="taxon:9606"
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Sequence 3 from Patent WO0170810.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         Denefle, P.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denef
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Pojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 4 08-NOV-2001;
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AK024328
AK024328.1 GI:10436685
Oligo capping; fis (full insert sequence).
Homo saplens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1002437.
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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomicseMri.co.jp, Tel:81-488-52-3951, Far:81-488-52-3952) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library Construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center ecc.) and Department of Virology, Institute of Medical Science,
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SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIV
ARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
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KEKLAAAERYLRSNNDILKPILMDVACDDIAHGQLTVPRSAAVAATGDAKPNMGRET
LLSICASVPRVEFHERHILEHFSFCVCVSYSLFPAKGIVSFSWASFRIWVLWRAVFWQ
HGESMAVWEGQLGLTSTTSLDVG"
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1 (bases 1 to 9634)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remaley, A., Brewer, H.B. and Dean, M.

Nucleic acids of the human abcl gene and their therapeutic and
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100.0%; Pred. No. 5.9e-114;
Live 0; Mismatches 0; Indels
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/clone_lib="PLACE1"
/note="cloning vector: pME18SFL3"
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AX127831
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/clone="PLACE1002437"
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Direct Submission
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121 TITCCCCGGTICIGITITCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAG 180
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1 (bases 1 to 9854)

Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C., Naudin,L., Lemoline,C., Duverger,N., Jaye,M., seaffoss Iii,G.H., Remaley,A., Brewer,H.B. and Dean,M.

Nucleics acids of the human abcl gene and their therapeutic and
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Patent: EP 1096012-A 70 02-MAY-2001;
    diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Sequence 70 from Patent EP1096012.
AX139818
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/db_xref="taxon:9606"
2219 c 2334 g 2635
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/db_xref="taxon:9606"
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VERSION
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1 (bases 1 to 10442)
Lawn, R.M., Wade, D. and Garvin, M.
Eawn, R.M., Wade, D. and Garvin, M.
Pegulation with binding cassette transporter protein abcl
Patent: WO 0078972-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 10442)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abcl polypeptides
Patent: Wo 0078971-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
a 2297 c 2408 g 2835
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AX060713
AX060713.1 GI:12406103
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AX060892
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2297 c 2408 g
AX060892.1 GI:12406270
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Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, Complete cds. AF285167.1 GI:9755158
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KLBPIATEVWLINKSMELLDBRKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT
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Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Briect Submission
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[ (bases 1 to 10442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwartz,K., Lawn,R.M. and Wade,D.P. ABCAl gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR
                                                                          2918 ggccgggacccgcagagccgacccttctctcccgggctgcggcagggcagggcgg 2977
                                                                                                                                                       2978 ggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgtttttccccg 3037
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                                                                                                                 1 GGCCGGGACCCGCAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
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        Length 10442;
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100.0%; Pred. No. 3e-102;
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1. .10442
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Best Local Similarity 100.(
Matches 197; Conservative
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SQLSGGMQPRLSVALAR-PEARLY TARGETSCHYPAREMEDIALVGLESSTAKANG
SQLSGGMQPRLSVALAR-PEARLY TARGET ILLST
HUMBADVLGDRIA I SHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLSSCRNS
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AVDGLALNFYEGQIPSELGSHRGAGKTTTMSILIGLEPPTSGTAYILGKDIRSBMSTIR
ONLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKTIR
FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLF
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PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
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I bases 1 to 10474)

Lawn,R.M., Wade,D. and Garyin,M.

Regulation with binding cassette transporter protein abcl
Patent: WO 0078972-A 7 28-DEC-2000;

CV THERAPEUTICS, INC. (US)

Location/Qualifiers

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Sequence 7 from Patent WO0078972.
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1 (bases 1 to 10474)

Lawn, R.M., Wade, D. and Garvin, M.

Lawn, R.M., Wade, D. binding cassette transporter protein abcl Patent: WO 0078972-A 9 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
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Pred. No. 5e-97;
0; Mismatches 0; Indels 0
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5.8%; Score 188; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5e-97;
Matches 188; Conservative 0; Mismatches 0; Indels 0
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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Sequence 9 from Patent W00078972.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 10474)

Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.

Patp binding cassette transporter protein abcl polypeptides

Patent: WO 0078971-A 7 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10474)

Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.

Atp binding cassette transporter protein abcl polypeptides

Patent: Wo 0078971-A 9 28-DEC-2000;

CV THERAPEUTICS, INC. (US)

Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-97;
Matches 188; Conservative 0; Mismatches 0; Indels
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Sequence 7 from Patent W00078971.
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/db_xref="taxon:9606"
2305 c 2416 g 2843
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/db_xref="taxon:9606"
2304 c 2415 q 2844
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Location/Qualifiers
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                             is updated, the accession number will
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26487: contig of 866 bp in length
26587: gap of 100 bp
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Direct Submission

L. Submitted (16-Jan-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
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Center: Whitehead Institute/ MIT Center for Genome Research
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      42 CCGCAGAGCCGAGCCTTCTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGGGAGGCTCC 101
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Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
ACC21345
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------ Project Information
Center project name: L4483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2439
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DEFINITION

AC021345

ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT

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36441 30540: gap or 100 bp 36541 37422: contig of 882 bp in length 37522: gap of 100 bp 37522: gap of 100 bp 38403 38602: contig of 880 bp in length 38403 38522: gap of 100 bp 39381 39480: gap of 100 bp 40408 40507: gap of 100 bp 40508 41406 41505: gap of 100 bp 41506 42399: contig of 894 bp in length 41505: gap of 100 bp 42400 42499: gap of 100 bp 42400 42499: gap of 100 bp 42500 43358 4357: contig of 899 bp in length 4357 4456: gap of 100 bp 4357 4456: gap of 100 bp 4457 4458: gap of 100 bp 4458 49393: gap of 100 bp 4538 49383: contig of 897 bp in length 49280: contig of 897 bp in length 49281 50350: contig of 897 bp in length 49381 50350: contig of 890 bp in length 50251 50350: gap of 100 bp 49381 50350: contig of 890 bp in length 50251 50350: gap of 100 bp 49381 50350: gap of 100 bp 49381 50350: gap of 100 bp 49381 50350: contig of 890 bp in length 50251 50350: gap of 100 bp 49381 50350: gap of
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66075: gap of 100 bp
66954: contig of 879 bp in length
67054: gap of 100 bp
67947: contig of 893 bp in length
68047: gap of 100 bp
68934: contig of 887 bp in length
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65015: cont
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaniai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)
Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Brewer,B., Duverior acid sequences of the abcl gene
Patent: WO 0183746-A 6 08-NOV-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
                                                                 10357 AAATCATGCTAGGAAAGATAACACCTTTTAATAACACTCTCTGCTTTTATAACATCATTC 10416
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                                        Gaps
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          Length 90698;
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Score 152; DB 2; Length yu. Pred. No. 5.1e-76;
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Best Local Similarity 100.0%; Pred. No. 5.4e-56;
Matches 117; Conservative 0; Mismatches 0;
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                                        0; Mismatches
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/db_xref="taxon:9606"
30 c 34 q 33
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Sequence 6 from Patent WO0183746.
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           Query Match
4.7%;
Best Local Similarity 99.2%;
Matches 252; Conservative
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synthetic construct
artificial sequence.
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REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

BASE COUNT

ORIGIN

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Homo sapiens
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9741)
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Patent; WO 0130848-A 69 03-WAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 9741)
Denefile,P., Rosler-Montus,M.F., Arnould-Requigne,I., Prades,C.,
Rawdin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Ili,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Mucleics acids of the human abcl gene and their therapeutic and
diagnostic application
Patent: EP 1096012-A 69 02-MAY-2001;
Aventis Pharma S.A. (FR)
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100.0%; Pred. No. 2.9e-41;
tive 0; Mismatches 0;
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        Sequence 69 from Patent WO0130848.
AX127830
AX127830.1 GI:14134477
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Sequence 69 from Patent EP1096012.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
2180 c 2290 g 2620
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Best Local Similarity 100.0
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1 (bases 1 to 446)

Denefielp., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C., Maudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Ili,G.H., Remaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human abcl gene and their therapeutic and diagnostic application
Patent: EP 1096012-A 3 02-MAY-2001;
Aventis Pharma S.A. (FR)

Location/Qualifiers
Denefle,P., Rosaler-Montus,M.F., Arnould-Reguigne,I., Prades,C., Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H., Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abcl gene and their therapeutic and
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/db_xref="taxon:32630"
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/db_xref="taxon:32630"
/note="Oligonucleotide Primer"
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                                                                                                       diagnostic application
Patent: WO 0130848-A 3 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Best Local Similarity 100.0
Matches 92; Conservative
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RESULT

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DEFINITION

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RESULT 33

AX127830

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PAT 30-MAY-2001

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Submitted (13-FEB-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (Deases I to 12628)

2 (Deases I to 12628)

Birren, B. Fasman, K. Lintcon, L., Nusbaum, C., Lander, B., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwall, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cackle, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Garalgery, K., Grant, G., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdord, A., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Molla, M., Morris, W., McGurk, A., McGernan, K., Maldrim, J., Molla, M., Morris, W., McGurk, A., McGernan, K., Mahdrim, J., Molla, M., Morris, W., Mourow, J., Mychalecky, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Stange-Thomann, M., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.

Submitted (O2-SEP-1998) Whitehead Institute/MIT Center for Genome Search, 320 Charles Street, Cambridge, MA 02141, USA on Sep 2, 1998 this sequence version replaced gi:3451370.

All repears were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker:html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Peter de Jong/ human PAC library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .640)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="HRPC843B9"
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Birren, B., Fasman, K., McKernan, C., Richardson, P.,
Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R.
Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P.,
Daly, M.J., Depayre, E., Devon, K., Dewar, K., Donelan, L., DuRette, B.,
Etemadi, S., Ferreira, P., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
Gensheimer, S., Geraigery, K., Gilmartin, T., Gray, D., Hagos, B.,
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MacKenzie, J., Marquis, N., McEwan, P., McGurk, A., Meldrim, J.,
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Ve, W.J., Zemtseva, I., Zhao, J. and Zody, M.
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Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abc1 gene Patent: WO 0183746-A 10 08-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 17, clone HRPC843B9, complete sequence
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100.0%; Pred. No. 2.9e-41;
tive 0; Mismatches 0; Indels
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone HRPC843B9
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                                                                                                                                                                   AX351038 9741 bp
Sequence 10 from Patent WO0183746.
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                  61 GAAAGAGACGCAAACACAAAAGTGGAAAACAG 92
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Best Local Similarity
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ORGANISM
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complement(25816, .25978)
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23606. .23899
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ACU21850 206966 bp DNA linear PRI 09-MAY-2001
Homo sapiens BAC clone RP11-389E17 from 4, complete sequence.
AC021850
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Waterston, R.H.
Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
4 (bases 1 to 206966)
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Submitted (16-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
5 (bases 1 to 206966)
Waterston, R.
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Sulston, J. E. and Waterston, R. Toward a complete human genome sequence
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Kang, K., Maupin, R. and Ureta, M.
The sequence of Homo sapiens BAC clone RP11-389E17
Unpublished
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Best Local Similarity 100.0%; Pred. No. 1.8e-25;
Matches 65; Conservative 0; Mismatches 0;
                                                                                                                                                                                     /rpt_family="Allogy"
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complement(35504 .35774)
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complement(32362. .32571)
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36517 3669
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AUTHORS

'rpt\_family="AT\_rich"

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenco, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEIGHBOAR DESCRING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-62B4. Actual start of this clone is at base position 1 of RP11-389E17; actual end is at base position 206966 of RP11-389E17.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping information for this clone was provided by Dr. John D. Morbherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
Direct Submission
Submitted (09-MRA-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 16, 2001 this sequence version replaced gi:11761497.
                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                   Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                               Center project name: H_NH0389E17
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/db_xref="taxon:9606"
/chromosome="4"
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531. .2753
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2987. .3022
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3223. .3260
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1779. 1908
/rpt_family="MIR"
1930. 1950
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1088. .1319
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Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abcal)
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Qlu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (14-JUL-2000) Genome Science Department, Lawrence Barkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Qlu,Y., Caveller, ... Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse abcal comparative sequencing and transgenesis studies revealing novel regulatory sequences Genomics 73 (1), 66-76 (2001)
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1016(87184 . 87402,103551 .103699,115064 .115187,

119217 .119358,120364 .120482,133479. 133400,

135582 .135758,147083 .147175,149791 .150031,

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160617 .160888,167790 .161994,162076 .163189,

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has 0; Indels
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35013. 35078
/rpt_family="AT_rich"
35645. 35691
/rpt_family="(CA)n"
36784. 37028
/rpt_family="L1"
37100. 337171
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40826. .41020
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34635. .34825
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39128. .39148
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37381. 37431
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Best Local Similarity 100.(
Matches 61; Conservative
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TITLE
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ANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFRAGLISPVARGFGCEYFALFEEQ
GIGYQWDNICHESPYBEDGFRILTANSSAMLEDTELKGWYTWITANYRDGMKVAY
DGLALNFYEGOITSFLCHNOAGKTTTWSILTGLEPPTSGTAY ILGKDIR SEBNSS TRON
LGYCPOQHNYLFDMLTVEEHIWFYARLKGLSEKHYKAEMEQMALDVGLPPSKLKSKTSO
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LQMLTGRNISDYLVKTYVQIIAKSIKNKIWYNEFRYGGFSLGVSNSQALPPSHEVNDA
IKQMKLLKLIKLTKSADRFLSSLGRFMAGLDTKNWKVWFNNKGWHAISSPLNVINNAIL
RANLQKGENPSQYGITAFNHPLNITKQQLSEVALMTTSVDVLVSICVIFAMSFYPASF
VVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYV
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MDADJULGNETALISHKKUVCSLSSLERKNOLGGTGYTJTLVKKUVESSLSCRRSST
VSCLKKEDSVSQSDAGLGSDHESDTLINSALSLTRKHVSEARLVEDIGHELTY
VLPYEAAKEGAFVELPHEIDDRLSDLOISSYGISETTLEEIFLKVAEESGVDAEFSDG
KLTQQQFVALLWRELIARRSPRGFTSDAVDNDSDIDPESRFIDLLSGMOGKGSYQLKGW
KLTQQQFVALLWRELIARRSRRGFTSDAVDLASPYVOIALVFSLIVPPFGKYPSLELD
PWMYNBQYTFVSNDAPEDMGTQBLLNALIKDRSFESDEN
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SLPRSTVDSLLQANVGLQKVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRK
KLDAAERVLRYNMDILKPVVTKLNSTSHLPTQHLAEATTVLLDSLGGLAQELFSTKSW
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ELFTNNKLNDINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW
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GGGONDILEIKELTKIYRRKRRPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGD
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GYTIVVRIAGSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILS
QSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQD
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87184. .210783
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173925. 174073,175605. 1175729,176761. 176859,180181. 180370,181179. 181273,182395. 118427,18398. 180370,181179. 181273,182395. 1182475,19351. 193808,196619. 196734,196845. 1996895. 1986734,196845. 1996895. 201051,201281. 201401,205277. 202558,205939. 2026842,207361. 207453,208135. 208378,209538. 210783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 57662)
                                                                                                                                                                                                                                                                                                                                ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                               0; Gaps
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Homo sapiens chromosome 11 clone CTD-2028015 map 11, LOW-PASS
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Contact: sequence_submissions@genome.wi.mit.edu
                                      255 others
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4.1e-23;
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                                                                                                                                                                                 Query Match 1.9%; Score 61; DB Best Local Similarity 100.0%; Pred. No. 4.1 Matches 61; Conservative 0; Mismatches
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AUTHORS
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\* NOTE: This record contains 73 individual

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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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                                                                                                                                                          718 817: gap of 100 bp 1525: contig of 708 bp in length 1526 1625; gap of 100 bp 1626 2265: contig of 640 bp in length
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9392: contig of 689 bp in length
9492: gap of 100 bp
10155: contig of 663 bp in length
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100 bp
13927: contig of 718 bp in length
13467: gap of 100 bp
1746: gap of 119 bc
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: contig of 688 bp in length

pap of 100 bp

: contig of 704 bp in length

pap of 100 bp

: contig of 707 bp in length
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27431: contig of 680 bp in length
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together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                     HS931E15
Human DNA sequence from clone 931E15 on chromosome Xq25. Contains
STSS, GSSs and genomic marker DXS8098, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGP/Chrx
931E15 is from the library RPCI5 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://Dacpac.med.buffallo.edu/ VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone 931E15.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Sep 18, 1998 this sequence version replaced gi:3550203. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neighbouring submissions.
The true left end of 424J12 (282213) is at 37431.
The true right end of 5052 (282213) is at 37431.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                      Oy 1187 ctgcccacttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
Db 39017 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGGCCCAGC 38960
                                                                                                                    Gaps
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702. .100?
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/note="Alusp repeat: matches 1. .302 of consensus"
1010. .1178
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                                                        Length 57662;
                                                                                                                    0; Indels
54444: contig of 679 bp in length
                                                                                         1.9e-21;
                                                        DB 2;
                                                        1.8%; Score 58; DB
ilarity 100.0%; Pred. No. 1.9
Conservative 0; Mismatches
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Direct Submission
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AL023575.1 GHG; DXS8098.
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Best Local Similarity
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JOURNAL
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KEYWORDS
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/note="FRAM repeat: matches 5. .166 of consensus"

Anote="Alli repeat: matches 1. .300 of consensus"
Afote="Alli repeat: matches 47. .276 of consensus"
B616. .8813
Anote="Alli repeat: matches 2. .121 of consensus"
R743. .8816
Anote="Alli repeat: matches 28. .301 of consensus"
R743. .8816
Anote="Alli repeat: matches 2. .300 of consensus"
R752. .9362
Anote="Alli repeat: matches 2. .300 of consensus"
R752. .9667
Anote="Alli repeat: matches 1. .302 of consensus"
R752. .9667
Anote="Alli repeat: matches 297. .919 of consensus"
R753. .3667
Anote="Alli repeat: matches 302. .301 of consensus"
R754. .11084
Anote="Alli R752. .2667
Anote="Alli R752. .301 of consensus"
R753. .11094
R754. .11084
R755. .11088
Anote="Alli R752. .301 of consensus"
R756. .11088
Anote="Alli R752. .301 of consensus"
R758. .11083. .11088
Anote="Alli R752. .301 of consensus"
R758. .11083. .11088 Anote="Aluyb repeat: matches 300. .1 of consensus" flote="Aluyb repeat: matches 2 . .302 of consensus" 5170. .5047

Anote="Li repeat: matches 3627 . .3966 of consensus" 5498. .5643

Anote="Alux repeat: matches 1 . .146 of consensus" 5644. .5948

Anote="Alux repeat: matches 1 . .301 of consensus" 5644. .5948

Anote="Alux repeat: matches 133. .290 of consensus" 5950. .6115

Anote="Alux repeat: matches 3365 . .4239 of consensus" 6059. .6979

Anote="Li repeat: matches 4377 . .4731 of consensus" 6078. .7073

Anote="MERZ repeat: matches 4.377 . .4731 of consensus" 6078. .7073

Anote="MERZ repeat: matches 345 . .284 of consensus" 7004="MERZ repeat: matches 345 . .284 of consensus" 7018. .7675

Anote="MERZ repeat: matches 345 . .284 of consensus" 7018. .7678

Anote="Alux repeat: matches 1 . .293 of consensus" 7018. .7960

Anote="Alux repeat: matches 5150 . .5270 of consensus" 8094 . .3936

Anote="Li repeat: matches 5150 . .5270 of consensus" 8094 . .3936

Anote="Alux repeat: matches 1 . .300 of consensus" 8094 . .3936 /note="Alusx repeat: matches 4. .302 of consensus" 12439. .12940 //note="LiMs2 repeat: matches 166. .685 of consensus" complement(13266. .13588) /note="match: STS L40936" /note="Aluxx repeat: matches 2. .302 of consensus" 1358. .14050 //note="Aluxy repeat: matches 1. .93 of consensus" 14055. .14323 //note="Aluxb repeat: matches 60. .301 of consensus" //note="Aluxb repeat: matches 60. .301 of consensus" /note="AluJb repeat: matches 13. .302 of consensus" 15126. .13428 /note="AluSx repeat: matches 1. .302 of consensus" 15626. .15730 complement(4220. .4537)
/note="AluJb repeat: matches 300. .1 of consensus" /note="AluSx repeat: matches 1. .300 of consensus" 2767. .3067 'note="AluJb repeat: matches 1. .302 of consensus" complement(1365. .1664) /note="match: STS G05254" 14514. .14836 repeat\_region misc\_feature misc\_feature

24520. .24884 /notca="L1PA5 repeat: matches 517. .890 of consensus" complement(25504. .25687) /notca="MER20 repeat: matches 155. .1 of consensus" 26421. .26649 /notca="32 copies 2 mer tt 83% conserved" complement(26486. 26661) /note="AluJb repeat: matches 196. .300 of consensus" 1618. .16420 /note="AluJb repeat: matches 1. .290 of consensus" complement(16828. .16935) /note="MER4B repeat: matches 11. .148 of consensus" 32041. 32319 /note="Alus: repeat: matches 1. .287 of consensus" complement(32381. 33599) /note="MLT2\_internal repeat: matches 4572. .3316 of complement(28817. .29089)
/note="Alusx repeat: matches 298. .2 of consensus"
29122. .29252
/note="Li repeat: matches 3151. .3280 of consensus"
complement(29957. .30200) complement(30513. .30706)
/note="MLT2\_internal repeat: matches 4754. .4572 of /note="FLAM\_A repeat: matches 117. .6 of consensus" complement(17160. .17224)
/note="MIR repeat: matches 149. .84 of consensus" 21550. .23628
Anote="putative CpG island"
complement(22542. .22581)
Anote="MIR2 repeat: matches 134. .95 of consensus"
complement(23094. .24185)
Anote="Sylva repeat: matches 1101. .1 of consensus"
24186. .24231 26867. 27164
/note="Alux repeat: matches 3.300 of consensus" 27165. 27462
/note="Alusp repeat: matches 2.302 of consensus" 28080. 283932
/note="Alusx repeat: matches 1.298 of consensus" complement(28817. 29089) 30728. .31025 /note="AluSx repeat: matches 1. .299 of consensus" 31059. .31356 /note="AluSy repeat: matches 1. .296 of consensus" 31359. .31505 (8120. .18226 /note="match: STS L24586" /note="match: GSSs B16853 B14990" /note="match: GSSs B16853 B14990" /note="match: GSSs B16853 B14990" /note="matches 303. .2 of consensus" /note="Alux repeat: matches 39. .298 of consensus" complement(20716. .20882) /note="MIR repeat: matches 260. .69 of consensus" complement(20824. .21385) /note="match: GSSs B94184 AQ010265" 33603. .33906 /note="AluJo repeat: matches 1. .302 of consensus" 34020. .34321 /note="AluJb repeat: matches 1. .301 of consensus" complement(34388. .34933) complement(26486, .26661)
force="Alaux repeat: matches 195, .5 of consensus" /note="MLT2\_internal repeat: matches 5375. .5124 /note="23 copies 2 mer aa 80% conserved" consensus consensus consensus repeat\_region misc\_feature misc\_feature misc\_feature misc\_feature

; Length 81874; 0; Indels Query Match 1.8%; Score 58; DB 9; Best Local Similarity 100.0%; Pred. No. 2e-21; Matches 58; Conservative 0; Mismatches 0 1187 ctgcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244

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Direct submission

Submitted (02-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk

ON Sep 27, 2000 this sequence version replaced gi:6006528.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone ame. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Swx: SWISSPROT; Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMPEP database can be found at their source databases:

better: An of the entire insert of clone RP1-247C2 it may be sequence is not the entire insert of clone RP1-247C2 it may be true left end of clone RP1-347C2 is at 1 in this sequence. The true left end of clone RP1-85M6 is at 4651 in this sequence. The true right end of clone RP1-85M6 is at 4651 in this sequence. The regions were either double-stranded or sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequence with it when it we have a prover the character because we sequence with it when alternate character because we sequence with an alternate character because which with munity data (i.e. physod munity or provered by high munity data (i.e. physod munity or provered by high munity data (i.e. physod munity or provered by high munity data (i.e. physod munity or provered by high munity data (i.e. physod munity or provered by high munity data (i.e. physod munity or provered by high munity data (i.e. physod munity data) is at physod munity or provered by high munity data (i.e. physod munity data (i.e. physod munity data) in this sequence.
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                                                                                                                                                                                    HSDJ247C2 98360 bp DNA linear PRI 03-AUG-2001
Human DNA sequence from clone RP1-247C2 on chromosome 11p13
Contains STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2191 of consensus"
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/note="L1PA11 repeat: matches 2180. .2215 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3216 of consensus"
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/note="LIAPA1 repeat: matches 3216. 6162 of consensus'
10697. 10906
/note="LIMEc repeat: matches 2142. 1979 of consensus"
Db 39890 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 39833
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/note="LiPAll repeat: matches 2154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1265. 5286
/note="L1PA11 repeat: matches 2215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="match: STS: Em:HS198YB10"
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VECTOR: pCYPAC2.
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/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .983)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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complement(45407. .45634)

complement(45407. .45634)

forte="match: GSS: Em:AJ247033"

53815. .53904

/note="Charlie2 repeat: matches 3272. .3370 of consensus"

54009. .54335

/note="Charlie2 repeat: matches 2888. .3117 of consensus"

56236. .57009

/note="L1PA2 repeat: matches 1. .776 of consensus"

7705. .62248

/note="L1PA2 repeat: matches 900. .6144 of consensus"

63508. .63541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42053. .42372
/note="Charliela repeat: matches 778. .1137 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40351. .40840
/note="Charliela repeat: matches 277. .769 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38956. .39215
/note="Charliela repeat: matches 28. .281 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: Em:AZ393320"
26106. .26561
/note="match: GSS: Em:AZ393320"
/note="LIMA8 repeat: matches 6175. .6268 of consensus"
33434. .33473
/note="LIMA8 repeat: matches 56. .98 of consensus"
complement(34597. .34987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Note="1.1983 repeat: matches 5743. .6147 of consensus" 37497. .37542 // Note="23 copies 2 mer tg 100% conserved" // Note="match: STS: Em:G45608" // Note="match: STS: Em:AU048503" // Note="match: STS: Em:AU048503" // Note="match: STS: Em:AU046429" // Note="match: STS: Em:AU046429"
/note="L1MEc repeat: matches 1978. .2279 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  17380. .17654
/note="MLT1A2 repeat: matches 92. .374 of consensus"
complement(17710. .18372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="17 copies 2 mer aa 82% conserved"
63586. .63668
/note="LIMD repeat: matches 738. .819 of consensus"
                                                                                                                                                                                                                                                                                                                                          /note="MLT1A2 repeat: matches 1. .92 of consensus"
                                                                                                                                                                                                             ρλ
                                                                                                    /note="LTR2 repeat: matches 1. .449 of consensus" complement(14642. .15322)
                                                                                                      complement(14642. .15322)
/note="match: GSS: Em:B04935"
15910. .15911
/note="Single clone region. Assembly confirmed lestriction digest data."
15930. .15955
/note="13 copies 2 mer tg 92% conserved"
                     13794, .13857
/note="32 copies 2 mer cc 68% conserved"
14618, .15078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38685. .38746
/note="31 copies 2 mer gt 91% conserved"
38956. .39215
                                                                                                                                                                                                                                                                                                                                                                                                                      complement(17710. .18372)
/note="match: GSS: Em:AQ485260"
18444. .18750
romptement(50477. .21170)
/note="match: GSS: Em:AQ488664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: 685: Em:AQ877394" 35999, 35984
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18685. 38746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(20761. .21177)
/note="match: GSS: Em:AQ669825"
complement(25626. .26158)
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25991. .26104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44071. .44491
/note="match: GSS: Em:AQ112832"
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2 [bases I to 145178]

8 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chasaro, B., Groke, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, Y., Devar, K., Devar, Y. S., Dodge, S., Faro, S., Faro, S., Fare, B., Porton, E., Hulme, M., Illev, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lancque, K., Lanczares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacCean, C., MacCean, C., MacCean, C., MacCean, C., Marguis, N., Matthews, C., McCarthy, M., Merwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, S., Strauss, N., Subramanian, A., Travers, M., Travers, M., Travers, M., Travers, M., Travers, N., Travers, M., Travers, N., Travers, N., Travers, N., Travers, N., Viel, Viel, N., Viel, N., Viel, N., Viel, N., Viel, N., Viel, Viel, N., Viel, N., Viel, N., Viel, Viel, Viel, Viel, Viel, Viel, N., Viel, N., Viel, N., Viel, Viel, N., Viel, N., Viel, 
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92079. 92237 /
/note="L1PA7 repeat: matches 5949. .6125 of consensus"
a 18802 c 18896 g 27671 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 18635 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 18578
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63917. .64021
/note="LIMD repeat: matches 984. .1089 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89057. .89594
/note="match: GSS: Em:AQ543464"
91625. .91990
/note="THELC repeat: matches 1. .371 of consensus"
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Pred. No. 2e-21;
0; Mismatches 0; Indels
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
                                                                                                                                                                                                                                            /note="match: GSS: Em:AQ277578" complement(76184. 76636) /note="match: GSS: Em:AQ812553" complement(76460. 76628)
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                                                           complement(64074. .65543)
/note="match: GSS: Em:AQ885350"
complement(66096. .66577)
                                                                                                                                                                                                                                                                                                                                                                                                     complement(76460. 76628)
//note==match: 6SS: Em.AQ140871"
complement(88581. 89052)
//note==match: GSS: Em:AQ201907"
                                                                                                                                                                   /note="match: GSS: Em:AQ611651"
69990. .70342
/note="match: STS: Em:G21603"
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Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 13, 2002 this sequence version replaced gi:18308666.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasKer.html
                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 48_0_9

Center clone name: 48_0_9

Sequencing vector: Plasmid; n/a; 100% of reads

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 144836 bases at least Q40

Consensus quality: 144952 bases at least Q20

Insert size: 141000; agarose-fp

Insert size: 144078; sum-of-contigs

Quality coverage: 18.7 in Q20 bases; sum-of-contigs

Quality coverage: 18.2 in Q20 bases; sum-of-contigs
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1. .68019
/note="assembly_fragment
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/db_xref="taxon:9606"
/chromosome="11"
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                                                                                     AC015494 146312 bp DNA linear HTG 26-MAY-2001
Homo sapiens clone RP11-21E12, WORKING DRAFT SEQUENCE, 12 unordered
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Birran, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-21E12
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 21_E15

Sequencing vector: Plasmid; n/a; 97% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 144580 bases at least Q40
Consensus quality: 144580 bases at least Q20
Insert size: 128000; agarose-fp
Insert size: 128000; agarose-fp
Ouality coverage: 9.4 in Q20 bases; agarose-fp
Ouality coverage: 9.4 in Q20 bases; agarose-fp
Ouality coverage: 9.3 in Q20 bases; agarose-fp
Ouality coverage: 9.3 in Q20 bases; agarose-fp
Sensists of 12 contigs. The true order of the pieces
Is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
Inus of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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center project Information
Center project name: L3990
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AC015494.6 GI:14209771
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                                                                                                                                DEFINITION
    43
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AUTHORS
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                                          AC015494
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RESULT
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AC015495 155982 bp DNA linear HTG 10-SEP-2000
Homo sapiens clone RP11-21E14, WORKING DRAFT SEQUENCE, 13 unordered
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contig of 1688 bp in length of 100 bp contig of 3882 bp in length
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/clone_lib="RPC1-11 Human Male BAC"
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/note="assembly_fragment
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/note="assembly_fragment"
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137496. .146312
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AC015495.4 GI:10047765
HTG; HTGS_PHASE1; HTGS_DRAFT.
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11527: con
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5857: gap of
7545: cor
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Matches 58; Conservative
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AUTHORS

REFERENCE TITLE AUTHORS

COMMENT

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                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dearx, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McKernan, K., Mcdonor, T., O'Connorl, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Connell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 10, 2000 this sequence version replaced g1:7249029. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155982)
Birren, B., Linfon, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-21E14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 21_E_14

Sequencing vector: M3; M77815; 100% of reads
Sequencing vector: M3; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.966731

Consensus quality: 147683 bases at least Q40
Consensus quality: 151981 bases at least Q30
Consensus quality: 153418 bases at least Q30
Insert size: 156000; agarose-fp
Insert size: 154782; sum-of-contigs
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Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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61396 61495: gap of
6136 65614: cont.
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11232 57436: conf
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                                                                                                                                                              Unpublished
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57437
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AC018988 157599 bp DNA linear HTG 26-DEC-2001 Homo sapiens chromosome 15 clone RP11-233C13 map 15, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
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1 (bases 1 to 157599)

Birran, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-233C13
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Db 9997 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 10054
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92174 92273: gap of 100 bp 92274 103879: contig of 11605 bp in length 103879 103978: gap of 100 bp 103979: gap of 100 bp 120092 120191: gap of 100 bp 120192 154009: contig of 13818 bp in length 154010 155982: contig of 1873 bp in length 154110 155982: contig of 1873 bp in length.
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49795 a 29060 c 29340 g 46582 t 1205 others
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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100.0%; Pred. No. 2.1e-21;
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KEYWORDS
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Demino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Porrest, C., Gage, D., Galagan, J., FatzHugh, W., Porrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, C., Wandon, J., Monnow, J., Marguis, N., Morow, J., Norman, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Sepencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tirrell, A., Sand, M., V., Wyman, D., Ye, W.J., Zimmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Submitted (25-DE0-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 26, 2001 this sequence version replaced gi:14010824.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L5451
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/db_xref="taxon:9606"
/chromosome="15"
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1.8%; Score 58; DB 2; Length 157599; 100.0%; Pred. No. 2.2e-21; ve 0; Mismatches 0; Indels 0;

Query Match 1.5%; Construction 1.0%; Pred. No. 2.2 Matches 58; Conservative 0; Mismatches

1187 ctgcccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244

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Db 145556 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 145613

Search completed: September 20, 2002, 06:25:43

Job time: 18137 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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		Description	Human ABC1 genomic	Nucleotide sequenc	Nucleotide sequenc	Human cDNA clone (	Human cDNA sequenc	Human ATP binding	Human ATP binding	Human cDNA clone (	Human cDNA sequenc
SUMMARIES			31	81	.03	29	51	56	115	32	90
SUMM			4F928	AF246	AF247	AH047	AH174	AD213	AAI70315	AH07432	AH18606
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		Score	814	541	541	336	336	228	228	217	217
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227 21 7086 22 7086 22 7281 22 9854 22 10442 22 10474 22 10474 22 10474 22 10474 22 235033 19 235033 19 237326 19	5351 22 8461 22 8319 22 10901 22 29329 22 29329 22 29329 22 149 21 425 22 17904 22 17904 22 17904 22 17904 22 17904 22 17904 22 17904 22	DNA; 1 rt entry r DNA.	OWO-IB01492 9US-0151977 0US-0526193 0US-0213958 IISH COLUMB NETICS INC. ks-Wilson A' /25.
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(HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
                                                                                                                                                                              Claim 8; Fig 1; 317pp; English.
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Ø The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCI expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.

Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;

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                                       782 atgaaacagaggcagaaagactttacgtaaattgctcatcatgtggttgtcaagtttgac
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25.2%; Score 814; DB 22; Length 183999; 99.7%; Pred. No. 0;
                      3; Indels
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Matches 964; Conservative
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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing streening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for

Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and

Claim 1; Page 143-144; 215pp; English.

atherosclerosis

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27451 ggcagctctctcatgccacctcattctggccaaaactcaggtcaaactgtgaagagtcta 27510
                                                                    27391 gcaggtggtgggagttctggaatatgatggagctggaggtgggaagagaagtaggcttgg 27450
                                                          aatytyaatctycccttcaayytygctacaaayytatctttytcaayytaygayacctty 1681
                   ggcagctctctcatgccacctcattctggccaaaactcaggtcaaactgtgaagagtcta 1621
                                                                                                                                                                                                                                                               Nucleotide sequence of the 5' flanking region of the human ABCl gene.
                                                                                                                                                                                                                                                                                   Human; adenosine triphosphate binding cassette protein 1; ABC1; pollipportein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                       AAF24681 standard; DNA; 1643 BP.
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99US-0153872.
99US-0166573.
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                                                                                                                                                                   2190 gtaagatgttcctctcgggtcctctgagggacctggggagctcaggctgggaatctccaa 2249
                                                                                                                                                                                                                                                                                are also useful as diagnostic indicators of cardiovascular disease and
                                                                                                                                                                                                                    ggcagtaggtcgcctatcaaaaatcaaagtccaggtttgtggggggaaaaacaaaagcagc 2309
                                                                                                                                                                                                                                                                                                                                                                   854 gtaagatgttcctctcgggtcctctgagggacctggggagctcaggctgggaatctccaa 913
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         1094 ccaatccetecetecegetgaggaaactaacaaaggaaaaaaaattgeggaaageagga
                                                                                                                                                                                                                                                                                                                                                                                                                   ccattacccagaggactgtccgccttcccctcaccccagcctaggcctttgaaaggaaac
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                                                                      Length 1643;
                                                                                             Indels
                                  Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other
       other disorders associated with hypercholesterolemia
                                                                     16.7%; Score 541; DB 22; L
100.0%; Pred. No. 1.2e-236;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF24703 standard; DNA; 1643 BP
                                                                     Query Match
Best Local Similarity 100.0
Matches 541; Conservative
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16-JUN-2000; 2000WO-US16591.

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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular chlosterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated
                                                                                                                                                                                                                  polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2190 gtaagatgttcctctcgggtcctctgagggacctggggagctcaggctgggaatctccaa 2249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other disorders associated with hypercholesterolemia.
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                                                                                                                                  Garvin M;
                                                                                                                                  Oram JF,
                              99US-0153872.
                                                                                (CVTH-) CV THERAPEUTICS INC (UNIW ) UNIV WASHINGTON.
              99US-0140264
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                                                                                                                                                                                                                                                      atherosclerosis
              18-JUN-1999;
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19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 541;
                                                                                                                                Lawn RM,
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Sequence 763 BP; 137 A; 205 C; 260 G; 158 T; 3 other;

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 3'-end sequence. Where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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Sugiyama T, Wakamatsu A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA clone (5'-primer) SEQ ID NO:1564.
                                                                                                                                                                                                                                                                                                                       AAH04729 standard; cDNA; 763 BP.
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11-JAN-2000; 2
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                                                                         Gaps
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           Length 763;
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Otsuki 1
           Score 336; DB 22; I
Pred. No. 4.1e-143;
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                                    Mismatches
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Sugiyama T, Wakamatsu A,
10.4%; Scc.
100.0%; Pre
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full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonolleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which complementary is a sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                           cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2956 gggctgcggcagggcagggcgggggagctccgcgcaccaacagagccggttctcagggcgc 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gggctgcggcagggcagggcgggggggggctccgcgcaccaacagagccggttctcagggcgc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 tacttgggcgttattgttttgtttcgaggccaaggaggcttcgggaagtgctcggtttcg 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 10.4%; Score 336; DB 22; Length 1750; Best Local Similarity 100.0%; Pred. No. 4.1e-143; Matches 336; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gggactttgatccggagccccacatccccaccatt 3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 gggactttgatccggagccccacatccccacctt 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the present invention.
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The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApcA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lober (IL-labeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid arthritis and septic shock. The present sequence is human ABC1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2887 aaaccccgtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccc 2946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3007 tcagggcgctttgctccttgtttttccccggttctgttttctccccttctccggaaggc 3066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2947 ttetetecegggetgeggeagggeagggeggggageteegegeaceaacagageeggtte 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ttctctcccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                         New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 aaaccccgtaattgcgagcgagagtgagtggggccgggagccgagagccgagccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ATP binding cassette transporter 1 (ABC1) cDNA.
              /product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI70315 standard; cDNA; 7260
                                                                                                                                     20-MAR-2000; 2000EP-0105820
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                                                                                                                                                                                                                                                           Schmitz G, Bodzioch M;
                                                                                                                                                                                                                                                                                                WPI; 2001-640388/74.
                                                                                                                                                                                                                   (FARB ) BAYER AG.
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                                                                                               26-SEP-2001.
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The present sequence is that of CDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AMENG217). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AA17014, using an alternative ATG codon as initiation codon and thereby adding an extra 40 N-terminal amino acids to the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in different Tangler kindreds. In the variant genes (numbering as in AA70314), G is changed to A at position 598 or G is changed to AA170114), G is changed to G at position 136, A is changed to G at position 2589 or G is changed to C at position 3456, or any combination of these. All of these polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589C) are both associated with a decreased in vitro ApoA-I mediated efflux of Cholesterol from mononuclear phagocytes, a mediated efflux of Cholesterol from mononuclear phagocytes, a mediated efflux of Cholesterol from mononuclear phagocytes, a mediated efflux of Cholesterol from mononuclear phagocytes, a cature typical of Tangier disease. 3 of the variants (G596A, A2589G and G3456C) are significantly increased in a population of man haring low high density lipoprotein-cholesterol levels and established coronary heart disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular erythematodes) is claimed. Modulation of ABC1 transcripts or proteins by antisense or ribozyme technology or RNA decoys is also protein and a subjects.
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "alternative open reading frame of AAI70314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
Tangier disease; coronary heart disease; diagnosis; gene therapy;
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                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace(2969,G)
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                                                                                                                                                                                                                                                         ..7106
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                                            polymorphism; ss.
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                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                 Key
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Length 7260; 7.1%; Score 228; DB 22; 100.0%; Pred. No. 7.7e-94; Query Match Best Local Similarity

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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence, where the
coligonucleotide comprises a 1'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                 aaaccccgtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccc 2946
                                                                                                       2947 ttctctcccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttc 3006
                                                                                                                                                                           tcagggcgctttgctccttgtttttccccggttctgttttcccccttctccggaaggc 3066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs ^{-}
                                                                                                                       Gaps
                                                                      1 aaaccccgtaattgcgagcgagagtgagtggggccgggacccgcagagccgagccgaccc 60
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                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA clone (5'-primer) SEQ ID NO:4267.
0; Mismatches
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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 Matches 228; Conservative
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27-AUG-1999;
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Ishii S,
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                                    2887
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       detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAM13618 and AAM13633 to AAM18742 represent human cDNA sequences; AAB92446 to AAM895893 represent human anino acid sequences; and AAM13629 to AAM13632 represent cliqonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                              2958 getgeggeagggeagggegggggageteegegeaceaacagageeggtteteagggegett 3017
                                                                                                                                                                                                                                                                                                                         tgetecttgtttttteeceggttetgtttteteecetteteeggaaggettgteaagggg 3077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                        getgeggeagggeagggeggggageteegegeaceaacagageeggtteteagggegett 124
                                                                                                                                                                                                                                          64
                                                                                                                                                                                       Gaps
particularly full-length cDNAs. The primers are also useful for the
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                                                                                                                                                           Length 736;
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                                                                                                                                                                                       0; Indels
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Otsuki
                                                                                                                   Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;
                                                                                                                                                         6.7%; Score 217; DB 22;
100.0%; Pred. No. 8.1e-89;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                              taggagaaagagacgcaaacacaaaagtggaaaacag 3114
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA sequence SEQ ID NO:18808.
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a T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH18606 standard; cDNA; 1556 BP
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02-MAY-2000; 2000JP-018776.
09-JUN-2000; 2000JP-018767
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                                                                                              the present invention.
                                                                                                                                                                                       217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
                                                                                                                                                                         Local Similarity
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                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH18606;
                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
AAH18606
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  833999993338
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The present invention describes primer sets for synthesising 5602

C full-length cDNAs defined in the specification. Where a primer set

C comprises: (a) an oligo-dr primer and an oligonucleotide complementary

C to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide sequences defined in the specification, where the

cligonucleotide comprises at least 15 nucleotides; or (b) a combination

C of an oligonucleotide comprising a sequence complementary to the

c complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 3'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, where the

polynucleotide comprises a 1'-end sequence, where the

cc polynucleotide comprises a 1'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, where the

cc polynucleotide which comprises a 1'-end sequence, polynucleotides,

cc particularly full-length cDNAs. The primers are also useful for the

cd etection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

cc AAH18732 to parsent human and no and a sequences; AAB93446 to

AAH95431 to part human and no and a sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2898 ttgcgagcgagagtgagtggggccggaccgcagagccgagccgaccttctctcccgg 2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgctccttgtttttccccggttctgttttctccccttctccggaaggcttgtcaagggg 3077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 gctgcggccagggcagggcggggggggctccgcgcaccaacagagccggttctcagggcgctt 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1556 BP; 380 A; 363 C; 399 G; 414 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%; Score 217; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 13690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3078 taggagaaagagacgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 8.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; chromosome mapping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC09615 standard; cDNA; 227 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1033401-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Dumas Milne Edwards J, Duclert A, Giordano J;

Claim 8; SEQ ID 18808; 2537pp + CD ROM; English

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                         Claim 1; SEQ ID 13690; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression and secretion vectors.
                       WPI; 2000-500381/45.
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2881 cggcaaaaaccccgtaattgcgagcgagtgagtgagtgggccgggacccgcagagccgagc 2940 0; Gaps cgaccottototocogggctgcggcagggcagggcggggagotccgcgcaccaacagagc 137 Similarity 100.0%; Pred. No. 1.3e-85; Conservative 0; Mismatches 0; Indels ( 3061 gaaggettgtcaaggggtaggagaaagaga 3090 Best Local Similarity 100.0 Matches 210, Conservative Query Match 78

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q δ q ò g

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Sequence 227 BP; 44 A; 65 C; 73 G; 45 T; 0 other;

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; himbibi, chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinfiammatcry; antiacthritic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                           Human ABCAl homologue-encoding cDNA, SEQ ID NO:976.
                                       ABA09200 standard; cDNA; 7086 BP.
                                                                                                                              11-JAN-2002 (first entry)
                                                                                    ABA09200;
RESULT 11
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0; Gaps

2910 gtgagtggggccgggacccgcagagccgagccgaccttctcccggggctgcggcaggg 2969

δ q δ

Homo sapiens.

Query Match 6.3%; Score 205; DB 22; Length 7086; Best Local Similarity 100.0%; Pred. No. 2.4e-83; Matches 205; Conservative 0; Mismatches 0; Indels 0,

Query Match

7 gtgagtggggccgggacccgcagagccgagccgaccttctctccccgggctgcggcaggg 66

2970 cagggcgggagctccgcgcaccaacagagccggttctcaggggcgctttgctccttgttt 3029

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control also relates to vectors and recombinant host cells and degrences ABBA0825-ABBA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of producing the nucleotides of producing the novel polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell contential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell contential therapeutic activities; stem cell growth factor activities; and hence thematopolesis regulatory activity; tissue growth activity; communomodulatory activity; activin. or inhibin-related activities; chemotactic or chemokinetic activities, haemostatic, thrombolytic activities, activities, pelpaptides or metastasis.

Communomodulatory activity; activities, polypeptides or may be compensing or an electric activities, pelpaptides and noncepensing, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy, such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions; e.g., myeloid or lymphoid cell varieties in sorterial isonaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and cell growth factor activity may be used to promote wound temporate acids encoding them) may be used to promote wound conditions and lugar and fungal infections in addition to immune disorders.

Colypeptides with growth factor activity may be used to promote cell gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                           Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 833-835; 1963pp; English.
                                                                                                                                                                                                                                                                                                    Tang YT, Liu C, Drmanac RT;
                                                                                                                            05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                    27-APR-2000; 2000US-0560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-457740/49.
                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABB11956
                       WO200157188-A2
                                                                                                                                                                          03-FEB-2000;
                                                                           09-AUG-2001.
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Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

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encoded polypeptides (AAM/8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mamunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                             3030 tttccccggttctgttttctccccttctccggaaggcttgtcaaggggtaggagaaagag 3089
                                                                cagggcggggagctccgcgcaccaacagagccggttctcaggggcgctttgctccttgttt 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ма
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Asundi V, Zhou P, Xu C,
Wang J, Zhang J, Ren F, Chen R, Wē
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 4558-4560; 6221pp; English.
                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 2196.
                                                                                                          AAK52667 standard; cDNA; 7086 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0496914.
2000US-0560875.
2000US-0598075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-064936.
15-SEP-2000; 2000US-064936.
30-OCT-2000; 2000US-0633251.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, E
Wang D,
Yang Y, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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01-SEP-2000;
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Zhao QA,
                                                                                                                                                                                                                                                           AAK52667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xue AJ,
                                                                                                                                                                                          12
                67
                                                                                                                                                                                                           AAK52667
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were missing at the time of publication

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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoies1s; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ma Y;
                                                                                                           2970 cagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgttt 3029
                                                                                                                                                                   tttccccggttctgttttctccccttctccggaaggcttgtcaagggggtaggaaagag 3089
                                                                                                                                                                                   67 cagggcggggggggctccgcgcaccaacagagccggttctcaggggcgctttgctccttgttt 126
                                                                               99
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities,
                                                      gtgagtggggccgggacccgcagagccgagccgaccttctctcccggggctgcggggg
                                                                                  Xu C, Cao Y,
R, Wang ZW;
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Length 7086;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rang YT, Liu C, Drmanac RT, Asundi V, Zhou P,
Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
6.3%; Score 205; DB 22;
100.0%; Pred. No. 2.4e-83;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1086-1096; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 228.
                                                                                                                                                                                                                          3090 acgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                      187 acgcaaacacaaaagtggaaaacag 211
                                                                                                                                                                                                                                                                                                                           AAK51683 standard; cDNA; 7281 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0496914.
2000US-056875.
2000US-0598075.
2000US-0620325.
200US-0654936.
2000US-0654936.
2000US-0693325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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15-SEP-2000; 2
20-OCT-2000; 2
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20-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                       AAK51683;
 Query Match
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                             Matches
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production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemanopodiasis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s M, Arnould-Reguigne I, Prades C, Naudin L;
Jaye M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                          Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                               2970 cagggcggggagctccgcgcaccaacagagccggttctcagggcgctttgctccttgttt 3029
                                                                                                                                                                                                                                                                                                                                45 gtgagtggggccgggacccgcagagccgagccgaccttctctcccgggctgcgggaggg 104
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                                                                                                 2910 gtgagtggggccgggacccgcagagccgacccttctctcccgggctgcggcaggg
                                                                                                                                                                                                                                                                                                                                                                                                                           tttccccggttctgttttctccccttctccggaaggcttgtcaaggggtaggaaagag
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                                                                                                                                                                                                                                        Length 7281;
                                                                                                                                                                                       Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                       6.3%; Score 205; DB 22;
100.0%; Pred. No. 2.4e-83;
7ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS06121 standard; cDNA; 9854
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Duverger N, Jaye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2000; 2000US-0186260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-2000; 2000WO-EP10886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-0402668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ABC1 DNA sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity
Matches 205; Conserv
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                                                                                                              inflammation
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Lemoine C,
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                                                                                                           The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological
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                                                                                                                                                                                                                                                                pathologies, and other diseases e.g. Tangier disease, lecithin
                                                                                                                                                                                                                                                                                                                                                            Length 9854;
                                New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes -
                                                                                                                                                                                                                                                                                                                Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                 cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                            6.3%; Score 205; DB 22;
100.0%; Pred. No. 2.4e-83;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of a human ABC1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "ABC1 polypeptide"
                                                                                Claim 1; Page 209-213; 368pp; English.
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P-PSDB; AAU02176.
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14-SEP-1999;
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                                                                                                                                                                                 useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
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                                                                                                                                                              Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
                                                                                                                                                                                                                                                                                                        present sequence encodes a human adenosine triphosphate (ATP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                Disclosure; Page 122-128; 215pp; English.
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                                                                                Garvin M;
99US-0166573
                                        (CVTH-) CV THERAPEUTICS INC
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                                                                                                                      WPI; 2001-137812/14.
                                                                                Lawn RM, Wade D,
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19-NOV-1999;
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binding casette protein (ABC) I polypeptide. ABC1 resides in cell
membranes and utilises ATP hydrolysis to transport a wide variety of
substrates across the plasma membrane. ABC1 is a pivotal protein in
the apolipoprotein-mediated mobilisation of intracellular cholesterol
stores. ABC1 is defective in Tanglar disease, a genetic disorder
characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
localised to chromosome 9422-9431. The ABC1 genes and proteins are
useful for developing pharmaceutical agents for the treatment of heart
disease and other disorders associated with hypercholesterolemia and
atherosclerosis. The genes are useful for developing screening assays to
screen for compounds that regulate the expression of genes associated
with cholesterol transport. The genes and proteins are also useful for
are also useful as diagnostic indicators of cardiovascular disease and
cother disorders associated with hypercholestarolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human adenosine triphosphate (ATP)
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100.0%; Pred. No. 1.1e-79;
tive 0; Mismatches 0;
                  /*tag= a
/product= "ABC1 polypeptide"
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                                                                                                                                                                                                                                                                                                             Garvin
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                                                                                                                                                                                                99US-0153872.
99US-0166573.
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                                                                                                                                             16-JUN-2000; 2000WO-US16591.
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Best Local Similarity 100.0
Matches 197; Conservative
291..7076
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                                                                       WO200078971-A2
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19-NOV-1999;
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a rangier disease patient. ABC1 resides in cell membranes and utilises ATP bydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                               Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                 Human; adenosine triphosphate binding cassette protein 1; ABC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
                                                                                                                                                                                                                                                            /product= "defective ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 148-154; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with hypercholesterolemia.
                                                                                                                                                                                                              Location/Qualifiers
323..7108
/*tag= a
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99US-0153872.
99US-0166573.
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                                (first entry)
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                                                                                                                                                                                Homo sapiens,
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 AAF24685;
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Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
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disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                  5.8%; Score 188; DB 22; Length 10474;
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                                                                                                                                                                                                                                                    Pred. No. 1.4e-75;
                                                                                                                                                                                                                                           100.0%; Prec. ...
                                                                                                                                                                                                                                                                           Conservative
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangler disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-Cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                                               Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "defective ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 170-176; 215pp; English.
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                                                                                                                                                                                           AAF24686 standard; DNA; 10474 BP.
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99US-0153872.
99US-0166573.
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                                                                     3107 gaaaacag 3114
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                                                                                                       222 gaaaacag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the
                                                                              2927 ccgcagagccgagccgaccttctcccgggctgcggcagggcagggcgggggagctccg 2986
                                                      Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                           Gaps
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         Length 10474;
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        5.8%; Score 188; DB 22;
100.0%; Pred. No. 1.4e-75;
iive 0; Mismatches 0;
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323..7108
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99US-0166573.
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                          Matches 188; Conservative
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P-PSDB; AAB31366.
                   Similarity
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          Query Match
                    Local
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plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
                     mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal FDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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/product= "defective ABC1 polypeptide"
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                                                                                                                                                                                                                                                                                                                                   associated with hypercholesterolemia.
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99US-0153872.
99US-0166573.
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14-SEP-1999;
19-NOV-1999;
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Garvin M;

Oram JF,

Wade D,

Lawn RM,

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The present sequence encodes a human adenosine triphosphate (ATP)
binding cassette protein (ABC) 1 polypeptide, and is isolated from
a rangier disease patient. ABC1 resides in cell membranes and utilises
ATP hydrolysis to transport a wide variety of substrates across the
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangier disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
9422-9431. The ABC1 genes and proteins are useful for developing
pharmaceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atherosclerois. The
genes are useful for developing screening assays to screen for compounds
that regulate the expression of genes associated with cholesterol
transport. The genes and proteins are also useful for are also useful
as diagnostic indicators of cardiovascular disease and other disorders
                                                               Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
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/*tag= a
/product= "Human ABC1 protein, amino acids 1 to 60"
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cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
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                                                                                                                                                   Claim 30; Page 165-172; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     associated with hypercholesterolemia.
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Matches 188; Conservative
                2001-137811/14.
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polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABCI gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                     Brewer HB;
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                                                                                                                                                                                                                                                                                                                                                       The sequence represents the partial coding sequence of human ABC1, which encodes amino acids 1-60 of the human ABC1 protein. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
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                                                                                                                                                                     Rosier-Montus M, Arnould-Reguigne I, Prades C,
Duverger N, Jaye M, Searfoss GH, Remaley A, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.8%; Score 92; DB 22; Length 446;
                                                                                                                                                                                                                                                                            New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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185..6967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS06120 standard; cDNA; 9741 BP
                                                                                         26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
                                                          26-OCT-2000; 2000WO-EP10886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ABC1 DNA sequence #1.
                                                                                                                                         (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
                                                                                                                                                                                                                                  WPI; 2001-316327/33.
                                                                                                                                                                                                                                               P-PSDB; AAU02176
WO200130848-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
                              03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2001
                                                                                                                                                                     Denefle P,
Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS06120;
                                                                                                                                                                                                       Dean M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
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RESULT 24
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                                                                                                                                                                                                                                                  The sequence represents the coding sequence #1 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                        Naudin L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3023 cttgtttttccccggttctgttttctccccttctccggaaggcttgtcaaggggtagga 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine butyrophilin; BT; human hereditary haemochromatosis; HFB; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                   Brewer HB
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis subregion from an unaffected individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                        Prades C,
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9741;
                                                                                                                     Rosier-Montus M, Arnould-Reguigne I, Prades (
Duverger N, Jaye M, Searfoss GH, Remaley A,
                                                                                                                                                                                                 New human ABC1 nucleic acids and polypeptides for treating
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 92; DB 22; Length 97. 100.0%; Pred. No. 8.6e-32; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3083 gaaagagacgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                               Claim 1; Page 204-208; 368pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV57926 standard; DNA; 235033 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type 1 sodium transport gene; ss.
                                          26-OCT-2000; 2000WO-EP10886.
                                                                26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US17658.
                                                                                                (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 92; Conservative
                                                                                                                                                               WPI; 2001-316327/33.
P-PSDB; AAU02176.
WO200130848-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                     03-MAY-2001
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                                                                                                                     Denefle P,
Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV57926;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                            Dean M;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV57926
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products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HK). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual comprising:

(b) providing DNA or RNA from the individual comprising:

(c) presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genotype indicates the likely products for use in the diagnosis and treatment of HFE. The present products for use in the diagnosis and treatment of HFE. The present protein butyrophilin (HT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a ROREt gene and antagonists of develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome, and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hereditary haemochromatosis subregion from an HH affected individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 225009 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 225063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                 Thomas WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Lv. 6.4e-15;
                                                                                                                                                                                     Lauer PM, Ruddy DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.7%; Score 55; DB
100.0%; Pred. No. 6.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarly be used for hypophosphatemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV57903 standard; DNA; 237326 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 1 sodium transport gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 8; 209pp; English.
97US-0852495
96US-0724394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0852495.
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                                                                                                                                                                                 feder JN, Kronmal GS, La
Fsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.79
Best Local Similarity 100.0
Matches 55; Conservative
                                                                                                             (PROG-) PROGENTIOR INC.
                                                                                                                                                                                                                                                                                           WPI; 1998-240014/21
07-MAY-1997;
01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolism
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us-09-846-456-1.oli.rng

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis (HFB) affected individual. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence of the haplotype genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The presence of the HFB gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFB. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a Robet gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and can can individual are homologues of a type 1 sodium transport gene, and can can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                            Hereditary haemochromatosis gene products – used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ribosomal S11 protein 12; cytostatic; virucidal;
immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
human immunodeficiency virus; HIV; infection; immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 227302 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 227356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1190 eccacettggceteccaaagtgetgggattacaggeatgagecactgegeecage 1244
                                                                                                                                                                                                                   present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 237326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                        Thomas WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "ribosomal S11 protein 12"
/note= "claimed in claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.4e-15;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.7%; Score 55; DB 19; Best Local Similarity 100.0%; Pred. No. 6.4e-15. Matches 55; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ribosomal S11 protein 12 encoding cDNA.
                                                          Ruddy DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarly be used for hypophosphatemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
643..969
                                                        Lauer PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI64613 standard; cDNA; 1316 BP
                                                                                                                                                                                     Claim 1; Fig 9; 209pp; English.
 96US-0724394.
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                                                        Feder JN, Kronmal GS, L.
Tsuchihashi Z, Wolff RK;
                             (PROG-) PROGENTIOR INC.
                                                                                                  WPI; 1998-240014/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200172801-A1.
01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                             metabolism
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Human; secreted extracellular matrix protein; ds; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzhelmers; immune/autoimmune disease; HIV infection; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic activity. The protein and encoding polynucleotide are used in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HYV) infection, immunological diseases and various inflammations. The polynucleotide is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                    applicable in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological disease; Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA for a novel extracellular matrix protein, Seq ID No 545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the human ribosomal $11 protein 12 with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human ribosomal S11 protein 12 and encoded polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 22; L
Pred. No. 1.5e-13;
0; Mismatches 0;
                                                                                                                 (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 29-30; 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Scc
illarity 100.0%; Pr
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS31466/c
ID AAS31466 standard; DNA; 5351 BP.
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20000S-0184664.
20000S-0186350.
20000S-0189874.
20000S-0190076.
26-MAR-2001; 2001WO-CN00438.
                                                          27-MAR-2000; 2000CN-0115182.
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                                                                                                                                                                                                                                     WPI; 2001-597104/67.
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                                                                                                                                                                                                                                                                       P-PSDB; AAG78169
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                                                                                                                                                                              Mao Y, Xie Y;
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16-MAR-2000;
17-MAR-2000;
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18 - APR-2000; 2000US-0198123.
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM

WPI; 2001-465572/50

Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -

Claim 1; SEQ ID No 545; 577pp; English.

The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical

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condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides compared as antigens to produce antibodies and to identify modulators of equoists and antagonists of the SPs. The anti-(SP) antibodies and cantagonists and antagonists of the SPs. The anti-(SP) antibodies and cantagonists and antagonists of the SPs. The anti-(SP) antibodies and contagonists and antagonists of the SPs. The anti-(SP) antibodies and contagonists include for example: immune/autoimmune diseases (e.g. HIV) (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis cand multiple sclerosis), cancers and hyperproliferative disorders (e.g. Marchiner's disease), neurological diseases (e.g. Alzhehmer's disease), neurological diseases (e.g. Alzhehmer's disease), previous articleors caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, sumple.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted extracellular matrix protein; ds; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; searcy syndrome; Gaucher; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
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07-JUL-2000;
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, medical, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be
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          agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists and antagonists of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of sp and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary tissues, modulation of for example
                                                                                                                                                                                                                                                       Gaps
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used as antigens to produce antibodies and to identify modulators
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Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 52; Conservative 0; Mismatches 0;
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2000US-0249213.
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Query Match 1.6%; Score 52; DB 22; Length 8319; Best Local Similarity 100.0%; Pred. No. 1.5e-13; Matches 52; Conservative 0; Mismatches 0; Indels

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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
Human reproductive system related antigen DNA SEQ ID NO: 5924.
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24-FEB-2000; 2000US-0184664.

22-MAR-2000; 2000US-0189874.

16-MAR-2000; 2000US-0189874.

17-MAR-2000; 2000US-0189874.

18-APR-2000; 2000US-01990176.

18-APR-2000; 2000US-0209467.

28-JUN-2000; 2000US-0209467.

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30-JUN-2000; 2000US-0215135.

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11-JUL-2000; 2000US-021647.

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14-AUG-2000; 2000US-0225214.

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                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                             olated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition .
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                             2000US-0250160.
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, harrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discrders e.g. Addison's disease, allerities, autoimmune harmony autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discrders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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Disclosure; SEQ ID NO 10357; 1701pp + Sequence Listing; English.
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1.6%; Score 52; DB 22; Length 29329;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0;
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08-DEC-2000;
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 12842; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative

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colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds. Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33324.

2000US-0184664. 2000US-0186350.

2000US-0179065

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17-MAR-2000;

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19-MAY-2000; 07-JUN-2000; 18-APR-2000;

30-JUN-2000;

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2000US-0189874 2000US-0198123 2000US-0205515 2000US-0214886 2000US-0215135

17-JAN-2001; 2001WO-US01354

WO200157182-A2. Homo sapiens.

09-AUG-2001.

AAK78512 standard; DNA; 29329 BP.

RESULT 33 AAK78512/ 07-NOV-2001 (first entry)

AAK78512;

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AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gane therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cyprucisor by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the complex of the nucleic acids into a host cell and culturing the cell to express the cadiagnose and freat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54912 to AAK54950 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 25603; 3071pp + Sequence Listing; English.
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Best Local Similarity 100.0
Matches 52; Conservative

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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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-NOV-2000;
                                                                                           26-SEP-2000;
27-SEP-2000;
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08-NOV-2000;
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25-SEP-2000;
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29-SEP-2000;
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13-OCT-2000;
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20-OCT-2000;
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20-OCT-2000;
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08-NOV-2000;
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08-NOV-2000;
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08-NOV-2000;
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17-NOV-2000;
                                                                      21-SEP-2000;
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02-OCT-2000;
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02-OCT-2000;
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20-OCT-2000;
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01-NOV-2000;
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cartivity, and can be used in gene therapy and vaccine production. (1)

activity, and can be used in gene therapy and vaccine production. (1)

proteins and polynucleotides may be used in the prevention diagnosis and

treatment of diseases associated with inappropriate (I) expression. For

example, they may be used to treat disorders associated with decreased

expression by rectifying mutations or deletions in a patient's genome

that affect the activity of (I) by expressing inactive proteins or to

supplement the patients own produce the secreted (I), by inserting

polynucleotides may be used to produce the secreted (I), by inserting

the nucleic acids into a host cell and culturing the cell to express the

protein. (I) proteins and polynucleotides may be used to prevent,

diagnose and treat immune/haematopoietic-derived cells. AAK64703

cancers and cancer metastases of haematopoietic-derived cells. AAK64703

concers and cancer metastases of haematopoietic antigen genomic

sequences from the present invention. AAK54942 to AAK54950 and AAM82169

represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 33324; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.6%; Score 52; DB 22; Length 29329; Best Local Similarity 100.0%; Pred. No. 1.5e-13; Matches 52; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein 5' EST, SEQ ID NO: 30024.
                                                                                                                                                                                                                                                                   Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC25949/c
ID AAC25949 standard; cDNA; 149
             2000US-0251030.
2000US-0251988.
2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251989.
2000US-0251989.
                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-2000 (first entry)
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             05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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EP1033401-A2

06-SEP-2000

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AA187958/c
ID AA187958 standard; cDNA; 425
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               2001-514838/56
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                           P-PSDB; AA001722
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                                                                            disorders
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                                                                                                                                                                                                      The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 51; DB 21; Length 149;
100.0%; Pred. No. 4.5e-13;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 149 BP; 37 A; 43 C; 40 G; 28 T; 1 other;
                                                                                    Duclert A, Giordano J;
                                                                                                                                                                                 Claim 1; SEQ ID 30024; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 1713.
                                                                                                                                                                                                                                                                                                                                                                       expression and secretion vectors.
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          21-FEB-2000; 2000EP-0200610.
                                   99US-0122487.
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similaring
                                                                                   Dumas Milne Edwards J,
                                                                                                           WPI; 2000-500381/45.
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                                                           (GEST ) GENSET
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                                   26-FEB-1999;
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019310) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
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Gaps

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08-NOV-2000;
08-NOV-2000;
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                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                     inflammation.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32733.
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0
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                                                                                                                                                                       Sequence 425 BP; 141 A; 83 C; 84 G; 116 T; 1 other;
                                                                                                                                                                                                                                                                                                         AAK77921 standard; DNA; 1856 BP
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2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0189874.
2000US-0190076.
2000US-0198123.
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2000US-0215135
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2000US-0209467
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2000US-0217487
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2000US-0220963
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2000US-0184664
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                                                                                                                                                                                                                                                                                                                                             07-NOV-2001 (first entry)
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 51; Conservative
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16-MAR-2000;
17-MAR-2000;
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14-JUL-2000;
26-JUL-2000;
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28-JUN-2000;
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07-JUL-2000;
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11-JUL-2000;
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24-FEB-2000;
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2000US-0241808.
2000US-0241809.
2000US-0241826.
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2000US-0246524
           14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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08-SEP-2000;
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02-OCT-2000;
13-OCT-2000;
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20-0CT-2000;
20-0CT-2000;
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20-0CT-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                          22-AUG-2000;
22-AUG-2000;
                                               18-AUG-2000;
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01-SEP-2000;
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21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
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02-OCT-2000;
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08-NOV-2000;
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08-NOV-2000;
14-AUG-2000;
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05-SEP-2000;
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12-SEP-2000;
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ANK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)

C amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)

C supplement the patients own production of (I). Additionally, (I)

C polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703

C cancers and cancer metastases of haematopoietic derived cells. AAK64703

C cancers and muman immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87650 and AAM82169

C represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 32733; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                           Human; polypeptide-cytochrome b5-13; malignant tumour; haemopathy; HIV; human immunodeficiency virus; infection; immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the human polypeptide-cytochrome b5-13 and its encoding polymuclectide. The polypeptide is used to treat various diseases, such as malignant tumour, haemopathy, human immunodeficiency virus infection, immunological diseases and various inflammation.
                            Gaps
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                                                                     Length 1856;
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                            Indels
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/note= "claimed in claim 6"
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                                                                                                                                                                                                                                   Human polypeptide-cytochrome b5-13 encoding cDNA.
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               4.4e-13;
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  DB 22;
1.6%; Score 51; DB 100.0%; Pred. No. 4.4 ative 0; Mismatches
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Matches 51; Conservative
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RESULT 3

Sequence 1856 BP; 375 A; 416 C; 358 G; 707 T; 0 other;

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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20000S-0198123.
20000S-0209467.
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-defice antigen genomic sequences from the present invention. AAK54942 to AAK87690 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidiaterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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  2000US-0256719
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Ruben SM; WPI; 2001-488786/53

The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB10743-ABB10980) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischammias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and or many or Human; reproductive system related antigen; reproductive system disorder; Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer -Gaps ; 0 Human reproductive system related antigen DNA SEQ ID NO: 6418. 1.6%; Score 51; DB 22; Length 17904; 100.0%; Pred. No. 4.4e-13; artive 0; Mismatches 0; Indels 0 Disclosure; SEQ ID NO 708; 577pp + Sequence Listing; English. Sequence 17904 BP; 5485 A; 3834 C; 3913 G; 4672 T; 0 other; ВР AAL03730 standard; DNA; 17904 2000US-0180628. 2000US-0184664. 2000US-0186350. 2000US-0189874. 2000US-0190076. 2000US-0198123. 2000US-0214886. 2000US-0215135. 2000US-0216647 2000US-0216880 2000US-0217487 2000US-0217496 2000US-0179065 2000US-0205515 2000US-0209467 17-JAN-2001; 2001WO-US01339 21-NOV-2001 (first entry) Query Match 1.6% Best Local Similarity 100.0 Matches 51; Conservative cancer; gene therapy; ds WO200155320-A2. 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; Homo sapiens. 28-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 07-JUN-2000; 31-JAN-2000; 02-AUG-2001 AAL03730; RESULT 41 AAL03730/ δ q 

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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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Query Match 1.6 Best Local Similarity 100. Matches 51; Conservative

Length 17904;

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Human; foetal tissue antigen; ds; antiinflammatory; neuroprotective; immunomodulator; cardiovascular; cytostatic; nephrothropic;
                                                                   cardiovascular; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; cancer; cardiovascular disorder; cardiac arrest; cerebrvascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; food additive.
Human DNA for a novel foetal antigen, SEQ ID No 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20000S-0226279.
20000S-0226681.
20000S-0226868.
20000S-0227182.
20000S-0227099.
20000S-0229287.
                                                                                                                                                                                                                                                                                                                                                                                                                  20000S-0189874.
20000S-0190076.
20000S-0198123.
20000S-0205515.
20000S-0205467.
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2000US-0216647.
2000US-0216880.
2000US-0217487.
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2000US-0225214.
2000US-0225266.
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20000S-0225270.
20000S-022547.
20000S-0225757.
20000S-0225758.
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2000US-0218290.
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2000US-0224519.
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                                                                                                                                                                                                   Homo sapiens.
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
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14-AUG-2000;
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21. SEP-2000; 2000US-02242474.

25. SEP-2000; 2000US-0234891.

26. SEP-2000; 2000US-0235834.

27. SEP-2000; 2000US-0235834.

29. SEP-2000; 2000US-0235836.

29. SEP-2000; 2000US-0235836.

29. SEP-2000; 2000US-0235836.

29. SEP-2000; 2000US-0236369.

29. SEP-2000; 2000US-0236369.

20. CCT-2000; 2000US-0236369.

20. CCT-2000; 2000US-0236369.

20. CCT-2000; 2000US-02363937.

20. CCT-2000; 2000US-0237039.

20. CCT-2000; 2000US-0241786.

20. CCT-2000; 2000US-0241786.

20. CCT-2000; 2000US-0241809.

20. CCT-2000; 2000US-0241809.

20. CCT-2000; 2000US-0241809.

20. CCT-2000; 2000US-0241809.

20. CCT-2000; 2000US-0246477.

08. NOV-2000; 2000US-0246477.

08. NOV-2000; 2000US-0246677.

08. NOV-2000; 2000US-0246677.

08. NOV-2000; 2000US-0246677.

08. NOV-2000; 2000US-0246670.

08. NOV-2000; 2000US-0246220.

17. NOV-2000; 2000US-0246220.
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2000US-0246611.
2000US-0249207.
2000US-0249208.
2000US-0249209.
2000US-0249209.
2000US-0249210.
2000US-0249211.
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2000US-0251030
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2000US-0233064
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17-NOV-2000;
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The invention relates to novel nucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also consist immunoassays e.g. radiolomnunoassays or enzyme linked include autoimment assays (ELISA). Disorders which are diagnosed or treated include autoimment diseases e.g. rheumatoid arthritis, whyerproliferative disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, or erebral ischaemia, angiogenesis, nervous system disorders e.g. cardiac arrest, or paperides can also conduct disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to respect that skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to respect that the stand other nutritional components. Numerous capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, cand other nutritional components. Numerous capabilities are given in the specification. The present sequence is a genomic DNA fragment from a gene encoding a foetal antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and
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Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human thioredoxin reductase (TxR) genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID No 1846; 642pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA53450 standard; DNA; 66566 BP
                                                                                                                                                                                                                                                                                          Rosen CA, Barash SC, Ruben SM;
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
11-DEC-2000; 2000US-0251990.
                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                    (XIAP)-binding protein), with thioredoxin reductase activity, useful e.g. for treating apoptosis-related disorders, cancer and inflammation
                                                                                                                                                                                                                                                                                               Thioredoxin reductase II (an X-linked inhibitor for apoptosis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 4.3e-13;
Live 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                    (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 74-135; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection. TxR can also be used screening of anti-cancer agents.
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                                                                                                              99WO-JP05983
                                                                                                                                                 98JP-0310422
                                                                                                                                                                                                                          Toji S, Yano M, Tamai K;
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Matches 51; Conservative
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gene therapy; ds
                                   WO200026382-A1.
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Homo sapiens.
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                                                                                                                                                 30-OCT-1998;
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The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-5, HDAC-D. These inhibitors may be antisense strands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and for identifying which histone deacetylase is involved in a neoplasia.
                                                                                     Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms of neoplasia, or for inhibiting neoplastic cell growth in an animal -
                                                                                                                                                                                                                                                                                                                                                                            Sequence 122186 BP; 29016 A; 31077 C; 32425 G; 29668 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 65150 ccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 65200
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Pred. No. 4.3e-13;
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100.0%; Pred. No. %...
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                                                                                                                                                                           Disclosure; Page 89-125; 125pp; English.
Macleod AR, Li Z, Besterman JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.69
Best Local Similarity 100.0
Matches 51; Conservative
                                            WPI; 2001-016407/02.
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Length 122186;

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September 20, 2002, 03:09:41; Search time 111.56 Seconds (without alignments) 7114.036 Million cell updates/sec
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.: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Sequence 20, Appl Description Sequence Seq Sequence Sequence Sequence Sequence Sequence US-08-724-394A-21 US-08-724-394A-22 US-09-128-15-17 US-08-471-570-9 US-08-975-080-35 US-09-630-706-10 US-09-499-884-11 US-08-973-544-1 US-09-167-681-37 US-08-367-841A-43 US-08-724-394A-20 US-08-724-394A-21 US-08-724-394A-22 US-08-323-443B-1 US-08-658-136-1 US-08-687-080-105 US-08-849-701-2 US-09-247-155-141 US-09-078-294-9 US-08-257-963B-12 US-08-367-841A-12 PCT-US95-07201-12 -08-724-394A-20 PCT-US95-07201-43 US-09-797-906-3 US-08-658-136-2 SUMMARIES % Query Score Match Length DB 1.7 246240 1.7 246240 1.5 31571 1.5 53526 1.5 53577 1.4 1701 1.4 3267 1.4 3267 1.4 3267 1.4 3267 1.4 3267 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.4 22481 1.7 22481 44444446666 Š. υυυ υv 000

, Appl , Appl Appli Appl Appl

Appl

Appli

21, Appl 22, Appl 1, Appli 1, Appli 105, Appli 105, Appli 141, App

NAME/KEY: misc\_feature | LOCATION: 1..246240 | OTHER INFORMATION: /note= "HLA-H.CONTIG" US-08-724-394A-20

Sequence 3, Appli Sequence 7, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 107, App Sequence 107, App		5872237el eto
US-09-496-694B-3 US-09-341-587-7 US-09-268-992-7 US-08-812-204-1 US-08-324-465-2 US-08-324-465-2 US-08-324-465-5 US-08-324-465-5 US-08-324-465-5 US-08-55-640-5 US-08-55-640-5 US-08-55-640-5 US-08-967-101-107 US-08-967-101-107 US-09-127-480-107 US-09-127-480-107 US-08-496-841C-103	ALIGNMENTS	/08724394A N. N. Gory S. M. Ton Ton Ton Ton Ton Ton Ton Ton Ton Ton
1.3 14796 4 0 1.3 72604 4 0 1.3 72604 4 0 1.3 1613 2 0 1.3 1656 1 0 1.3 1656 2 1 0 1.3 1656 5 P 1.3 1725 1 0 1.3 1725 2 0 1.3 1725 5 P 1.3 1725 5 P 1.3 198 2 0 1.3 198 4 0 1.3 198 4 0		ication US/08  TON: Omal, Gregor Omal, Gregor Omal, Gregor Omal, Gregor Omoribashi, Ze Iff, Roger K. TION: Megaba TION: Me
C 328 331		NESULT 1  US-08-724-394A-20/C Sequence 20, Applicat Sequence 20, Applicat Patent No. 5872237 GENERAL INFORMATION: APPLICANT: Feder, APPLICANT: Thomas APPLICANT: Thomas APPLICANT: TWO 1ff, TITLE OF INVENTION UNMBER OF SEQUENCE CORRESPONDENCE ADD ADDERSSEE: TOWN STREET: TWO EMT CITY: San Franc STATE: CA COMPUTER READABLE MEDIUM TYPE: Fl COMPUTER: IBM FOREATING SYSTER SOFTWARE: PATER COMPUTER: IBM FOREATING SYSTER COMPUTER: IBM FOREATING SYSTER SOFTWARE: PATER COMPUTER: IBM FOREATING SYSTER SOFTWARE: PATER COMPUTER: IBM FOREATING SYSTER SOFTWARE: PATER COMPUTER: IBM FOREATING SYSTER SOFTWARE: FILLS TELECOMMUNICATION TELECOMUNICATION TELECOMMUNICATION TELECOMMUNICATION TELECOMMUNICATION TELECOMUNICATION TELEC

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US-08-724-394A-22/C
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                                                                                                                                              Db 14447 CCCACCTTGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 14393
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                               Query Match 1.7%; Score 55; DB 2; Length 246240; Best Local Similarity 100.0%; Pred. No. 5.1e-15; Matches 55; Conservative 0; Mismatches 0; Indels 0
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Sequences and Antibodies Thereto
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100.0%; Pred. No. 5.1e-15;
Live 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REPERENCE/DOCKET NUMBER: 017957-000100
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   Sequence 21, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
GAPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                              Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                            Lauer, Peter M. Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                            Kronmal,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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US-08-724-394A-21/C
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        1190
        cccacttggcctcccaaaqtgctggattacaggcatgagccactgcgcccagc
        1244

        Db
        14447
        CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC
        14393

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 246240;
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APPLICATION NUMBER: US/08/724,394A
FILING DATE: U0-0CT-1996
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: Fitts, Renea 35,136
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYCYSTIC KIDNEY DISEASE GENE
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100.0%; Pred. No. 5.1e-15;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc_feature

) LOCATION: 1..246240

) OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                            STAIL:
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--verter: IBM PC compatible
--verter: IBM PC compatible
--verter: IBM PC compatible
Sequence 22, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Taudy, David A.
APPLICANT: Tauchinashi, Zenta
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
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APPLICANT: LANDES, GREGORY M.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
TITLE OF INVENTION: POLYCYSTIC KID
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; Patent No. 5654170
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant
not relevant
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Best Local Similarity 100.C
Matches 55; Conservative
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STRANDEDNESS: not r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-323-443B-1
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RESULT

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31,845
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 53577 base pairs
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: ONE MOUNTAIN
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: LANDES, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY C
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.5%; Score 48; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.5e-12;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFRENCE/DOCKET NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAYAME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08658136 Patent No. 6071717 GENERAL INFORMATION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MASSACHUSETTS
USA
                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-658-136-2
                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KLINGER, KATHERINE WAPPLICANT: KLINGER, GREGORY MAPPLICANT: LANDES, GREGORY MAPPLICANT: LANDES, GREGORY MAPPLICANT: GLANDES, TIMOTHY DAPPLICANT: GREGORY MAPPLICANT: GREGORY GREGORY GREGORY GREGORY GREGORY GREGORY GREGORY GREGORY GREGORY FOR INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                            REFERENCE DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPAX: 508-872-8400
TELEPAX: 508-872-8415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 51526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGIETRATION NUMBER: 31,845
REFRENCE/DOCKET NUMBER: GEN4
TELECOMMULCATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-658-136-1; Sequence 1, Application US/08658136; Patent No. 6071717
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Gaps

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US-08-849-701-2/C
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                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
                                                                                                                                                ;
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0
                                                                                              Query Match 1.5%; Score 48; DB 3; Length 53577; Best Local Similarity 100.0%; Pred. No. 6.3e-12; Matches 48; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                         5' END OF INTRON 21 OF RAD50 GENOMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
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REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SED ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 13158 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.96
Matches 47; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Sulte 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JRN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   Sequence 105, Application US/08687080 Patent No. 5965427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1
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; INDIVIDUAL ISOLATE:
US-08-687-080-105
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MOLECULE TYPE:
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ZIP: 94306
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US-08-687-080-105
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1: 620 Newport Center Drive 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Ducqueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET. 021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/094,121
EARLIER APPLICATION NUMBER: 60/094,563
EARLIER APPLICATION NUMBER: 60/091,563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
                                                                APPLICANT: Miyai, Kiyoshi
APPLICANT: Naitoh, Tsutomu
APPLICANT: Noekawa, Toshihiro
ITILE OF INVENTION: Method of Cell Detection
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02734
FILING DATE: 27-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 141, Application US/09247155A
; Patent No. 6312922
; Sequence 2, Application US/08849701; Patent No. 5922544; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 153 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                               COUNTRY: U
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APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PICHENT EPITHELLUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
ANDRESPONDENCE ADDRESS:
ADDRESSES ADDRESS:
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Sequence 12, Application US/08367841A
Sequence 12, Application US/08367841A
Sequence 12, Application US/08367841A
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Ignacio R.; Mazuruk, Joyce
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 3.3 kb PCR product OTHER INFORMATION: using primers, SEQ ID No. 5840686 15 and
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1.4%; Score 45; DB 2; Length 3267;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
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STREET: 345 Park Avenue
                                                                                                                                                                                             ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952;
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPRAX: (212) 758-4800
TELEPRAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEGUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Genomic DNA FEATURE:
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TYPE: Nucleic Acid
STRANDEDNESS: Double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                             New York
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                                                                                                                                                                                                                    STREET: 345 Par
                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCEEC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 4..447
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 4..147
OTHER INFORMATION: VON Heijne matrix
OTHER INFORMATION: score 5.6999980926514
OTHER INFORMATION: seq_LLLFFGKLLVVGG/VG
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08257963B
Patent No. 5840686
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
                         EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 141
LENGTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09078294
Patent No. 6265211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.4%
Best Local Similarity 100.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: BAC-F2 contig 5
US-09-078-294-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: polyA_signal
LOCATION: 858..863
FEATURE:
                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: polyA_site
; LOCATION: 880..891
US-09-247-155-141
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US-08-257-963B-12
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LENGTH: 1701
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US-09-078-294-9
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1033 aacctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1077
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LENGTH: 3663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ); OTHER INFORMATION: 3.3 kb PCR product
; OTHER INFORMATION: using primers, SEQ ID No. 6319687 15 and 16
US-08-367-841A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application PC/TUS9507201
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVEDE FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
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1.4%; Score 45; DB 4; Length 3267;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NOMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                              20264126US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 2026412
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
TYPE: Nucleic Acid
STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 345 Park Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy I
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: JT109
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                 USA
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Sequence 11, Application US/09499884

Patent No. 6265172
GENERAL INFORMATION:
APPLICANT: St. Clair, Daret
APPLICANT: Urano, Muneyasu
APPLICANT: Wasarskis, Edward
TITLE OF INVENTION: ASSOCIATED DISEASES
FILE REFERENCE: 50229-180
CURRENT FILING DATE: 1000-02-08
CURRENT FILING DATE: 2000-02-08
CURRENT FILING DATE: 2000-02-08
CURRENT FILING DATE: 2000-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | IDENTIFICATION METHOD:
| OTHER INFORMATION: 3.3 kb PCR product
| OTHER INFORMATION: using primers, SEQ ID No: 15 and 16
| PCT-US95-07201-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccac 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 CCCACCTTGGCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 45; DB 5; L6
100.0%; Pred. No. 1.5e-10;
tive 0; Mismatches 0;
                                 APPLICATION NOTE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 BASE PAIRS
TYPE: NUCLEIC ACID
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-499-884-11
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TOPOLOGY: Unknown
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Gaps

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Indels

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0; Mismatches

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Query Match 1.4%; Score 45; DB 4; Length 5581; Best Local Similarity 100.0%; Pred. No. 1.5e-10;
                                                                                                                                                                                                                                              ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth St., NW, Sulte 300, G St. Lobby
                                                                                                                                                                APPLICANT: WEISS, Elisabeth
TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
1970 AACCTCTGCCTCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCC 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PAIGHT, RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,544
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT EP 96/02663
FILING DATE: 20-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICEATION NUMBER: EP 95109511.6
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112201.9
FILING DATE: 03-AUG-1995
ATTORNEY, AGENT INFORMATION:
NAME: Kitts, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P8341-7073
TELECOMMNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P8341-7073
                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     Sequence 1, Application US/08973544 Patent No. 6338950 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5581 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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2325..2709
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COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
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1775..1797
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1475..1567
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LOCATION:
                                                                RESULT 15
US-08-973-544-1/c
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US-08-367-841A-43
US-08-367-841A-43
Sequence 43, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Tignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGRANT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
UNMBER OF SEQUENCES: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Diane M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REPERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PASLSEQ for Windows Version 3.0
                                                                                                                                                                      ; Sequence 37, Application US/09167681A; Patent No. 6265561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (6309)...(6404)
NAME/KEY: CDS
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (3730)...(3879)
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CDS
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US-09-167-681-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 37
LENGTH: 8397
                                                                                                                                      RESULT 16
US-09-167-681-37
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
NAME/KEY:
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Matches
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FOCT-USS5-07201-43

Sequence 43, Application PC/TUS9507201

Sequence 43, Application PC/TUS9507201

APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Particla; Schwartz, Joan P.;

APPLICANT: Particla; Schwartz, Joan P.;

APPLICANT: Particla; Schwartz, Joan P.;

TITLE OF INVENTION: PIGMENT EPITHELIUM

TITLE OF INVENTION: OF SEQUENCE OF THE PEDF GENE

TITLE OF INVENTION: OFGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
) OTHER INFORMATION: full length genomic
) OTHER INFORMATION: sequence for PEDF plus flanking sequences.
US-08-367-841A-43
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1.4%; Score 45; DB 4; Length 22481;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                 20264126US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA.
APPLICATION NUMBER: PCT/US95/07201
FILLING DATE: 06-UUN-1995
                                                                                                                                  FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SED-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy Disk
IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 22481 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDA.
STREET: 34.
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: P1-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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GENERAL INFORMATION:
APPLICAMT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY; TILLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TILLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TILLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: full length genomic OTHER INFORMATION: sequence for PEDF plus flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.4%; Score 45; DB 5; Length 22481; Best Local Similarity 100.0%; Pred. No. 1.4e-10; Matches 45; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 84495;
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100.0%; Pred. No. 1.3e-10;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 17174 CCCACCTTGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 17218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                              20264126PCT
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CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION.

NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 759-6849
INFORMATION POR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/09797906
; Patent No. 6329188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COTHER INFORMATION: n = A,T,C or GUS-09-797-906-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: P1-147
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-07201-43
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Ouery Match Best Local Similarity 100.0\$; Score 45; DB 2; Length 246240; Best Local Similarity 100.0\$; Pred. No. 1.2e-10; Matches 45; Conservative 0; Mismatches 0; Indels 0
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
FELEPRACE DOCKET NUMBER: 017957-000100
TELEPRA: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
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Sequence 22, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                              APPLICANT: Thomás, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 242021 AACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCC 242065
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ZIP: 94111-384

ZIP: 94111-38 FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DoS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
ATTONNEY/AGENT INRORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Pattent No. 5872237
; GENERAL INFORMATION:
                                                                                                         Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                                                  Feder, John N.
Kronmal, Gregory S.
Lauer, Peter M.
Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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                                                                                       US-08-724-394A-20
                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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Gaps ; 0

No. 5872237el

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Length 2310;
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                       Db 45158 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGC 45115
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IGARASHI, KOichi
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, Tatesuya
APPLICANT: WATANABE, TATESUY
APPLICANT: WATANABE, TATESUY
APPLICANT: WATANABE, TATESUY
APPLICANT: WATANABE, TATESUY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 1.3%; Score 43; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE:
APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AGG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, ETNEST V
REGISTRATION NUMBER: 29822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/08471570 ; Patent No. 5750371
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; Sequence 7, Application US/08471570
; Patent No. 5750371
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: IGARASHI, KOICHI
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, TATESUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)523-6440
TELEEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 2310 base pairs
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EDNESS: double
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                                                                                                                  RESULT 24
US-08-471-570-9/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Fatent No. 6177654
GENERAL INFORMATION:
ABPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 18
SOFTHANE: FRALER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
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1.4%; Score 44; DB 3; Length 176373;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION DARA:
APPLICATION NUBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLEASTFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
TELEPHONE: 415-576-020
TELEFANG 415-576-020
TELEFANG 415-576-030
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
"WITH TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO TEMPLO
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LOCATION: 1..246240

CTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-5948-22
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; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: not relevant not relevant
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: not rele
MOLECULE TYPE: CDNA
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US-09-128-155-17/c
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APPLICATION NUMBER: US/08/975,080 FILING DATE: 20-NOV-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/031,435 FILING DATE: 20-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 10, Application US/09630706
; Patent No. 6277640
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) US-08-975-080-35
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-630-706-10
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NAME/KEY: CDS
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NAME/KEY: CDS
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Best Local Similarity
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LOCATION: (281:
NAME/KEY: CDS
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TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
GORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2676;
                                                ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Le
1.1e-09;
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
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1.3%; Score 43; DB Best Local Similarity 100.0%; Pred. No. 1.1
Matches 43; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/743369
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/08975080 Patent No. 6245523 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (61)7573-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29822
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: US 07
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LINEK, Ernest V
REGISTRATION NUMBER: 2
                                                                                                          CITY: Boston
STATE: Massachusetts
                NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25..2331
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                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 26
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Gaps
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APPLICANT: C. Frank Bennett
APPLICANT: Lex M. COWSERT
TILLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
FILLE REPERENCE: RTS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1035 cctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1077
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100.0%; Pred. No. 1e-09;
tive 0; Mismatches (
                                                                                                                                                                 NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEPRAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
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ADDRESSEE: FOLEY, HOAG & ELIOT LLP STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, or t
US-09-268-992-7
             Sequence 7, Application US/09268992
Patent No. 6342351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MI.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 7
LENGTH: 72604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-812-204-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                            APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric E. Swayze
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 1090-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
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Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 43; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.3%; Score 43; DB ABest Local Similarity 100.0%; Pred. No. 1e-Matches 43; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
Sequence 3, Application US/09496694B Patent No. 6335194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09341587
Patent No. 6346606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (5158)...(5275)
NAME/KEY: CDS
: LOCATION: (11955)...(12044)
US-09-496-694B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7
                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 28720
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Gaps
APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

CURRENT APPLICATION NOBER: US/08/812,204
FILING DATE: 06-MAR.1997

FILING DATE: 06-MAR.1997

FILING DATE: 06-MAR.1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy 1199 gcctcccaaagtgctgggattacaggcatgagccactgcgccc 1241
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Patent No. 5965790
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: THERAPEUTIC METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.3%; Score 43; DB 4; Lo
Best Local Similarity 100.0%; Pred. No. 9.6e-10;
Matches 43; Conservative 0; Mismatches 0;
                                                                                                    FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER APPLICATION NUMBER: 60/008,312
EARLIER FILING DATE: 1998-10-28
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTHARE: FASTSEQ for Windows Version 3.0
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34,819
R: 00530/065002
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/465,981
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,465
FILLING DATE: October 17, 1994
APPLICATION NUMBER: 07/999,742
FILLING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 225 Franklin Street CITY: Boston STATE:
                                           ; Sequence 2, Application US/08465981
; Patent No. 5874415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617) 542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                        Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US93-11915-2
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                             US-08-465-981-2
                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                    Length 1613;
                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: GENE TRANSCRIPTION AND
TITLE OF INVENTION: IONIZING RADIATION: METHODS
TITLE OF INVENTION: AND COMPOSITIONS
                                                                                                                                                    Query Match 1.3%; Score 42; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPRONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08324465
Patent No. 5565334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Fish & Richardson
225 Franklin Street
                                                               TOPOLOGY: linear;
MOLECULE TYPE: DNA (genomic)
US-08-812-204-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 1613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1656
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Best Local Similarity 100.
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-324-465-2
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GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Abe, Miyaba
TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 42; DB 2; L6 100.0%; Pred. No. 3.2e-09; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/08324465
; Patent No. 556334
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abe, Miyako
TITLE OF INVENTION: GENE TRANSCRIPTION AND
TITLE OF INVENTION: IONIZING RADIATION:
TITLE OF INVENTION: AND COMPOSITIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,465
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPROXE. 10617) 542-8906
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065001
                                                                                                                                                            APPLICATION NUMBER: PCT/US93/11915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/999,742
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                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
PCT-US93-11915-2
                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 225 Fr
CITY: Boston
STATE: Massach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08465981

Patent No. 5874415

GENERAL INFORMATION:
APPLICANT: Rufe, Donald
APPLICANT: Abe, Miyako
TITLE OF INVENTION: ENPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                            1040 gcctcccgggttcaagcgattctcctgcctcagcctcctgag 1081
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,465
FILING DATE: October 17, 1994
APPLICATION NUMBER: 07/999,742
FILING DATE: December 31, 1992
ATORNEY AGENT INFORMATION:
NAME: Fraser, Janis K.
RECISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617),542-5770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,981
TELECOMMUNICATION INFORMATION:
                TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEEX: 200154
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617) 542-8906
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                                                                                                                                                        nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
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STRANDEDNESS: double
                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-324-465-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-465-981-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-465-981-5
                                                                                                                                     LENGTH:
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1036 ctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1077
                                               COMPUTER READSLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFFCATION: 435
                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                20005-3918
D.C.
Y: USA
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US-09-050-159-129
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LENGTH: 5590
                      COUNTRY:
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                                                                                                                                                                                                                           MODULATING
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Sequence 5, Application US/08655640
Sequence 5, Application US/08655640
Sequence 5, Application US/08655640
Sequence 5, Application US/08655640
SEPLICANT: Teng, Christina APPLICANT: Panella Timothy J. APPLICANT: Panella Timothy J. APPLICANT: Panella Timothy J. APPLICANT: CONTRESPONDENCE SEQUENCES: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
                                                                                                                                            Sequence 5, Application PC/TUS9311915
GENERAL INFORMATION:
APPLICANT: Kufe, Donald
APPLICANT: Kufe, Donald
APPLICANT: BAG, MIYANO
TITLE OF INVENTION: ENPRANCER SEQUENCE FOR MODULATI
TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 42; DB 5; L
100.0%; Pred. No. 3.1e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/065W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFRA: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/999,742
FILLING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                   Boston
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PCT-US93-11915-5
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                                                                                                                 RESULT
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; Sequence 129, Application US/09050159A
; Patent No. 6197505
; GENERAL INFORMATION:
    APPLICANT: No. 6197505berg, Leif T
    APPLICANT: Andersson, Maria K
; APPLICANT: Linstrom, Per H
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/050,159A
; CURRENT FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/042,930
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Length 2086;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%; Score 42; DB 2; Length 208 Best Local Similarity 100.0%; Pred. No. 3.1e-09; Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1195 cttggcctcccaaagtgctgggattacaggcatgagccactg 1236
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WTS/5683/98019/SAP
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LENGTH:
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                                                                                                                                                                              APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
TITLE OF INVENTION: GREATIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISBASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 107, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 198;
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1837 ctctgcctcccgggttcaagcgattctcctgcctcagcctcc 1878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 CCTTGGCCTCCCAAGTGCTGGGATTACAGGCATGAGCCAC 52
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1.3%; Score 41; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   Sequence 107, Application US/08967101
Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7100 TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-967-101-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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02110
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                                                                                                                                                              GENERAL INFORMATION:
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                                                                                           US-08-967-101-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-592-541-107
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                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1194 ccttggcctcccaaagtgctgggattacaggcatgagccac 1234
                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.3%; Score 41; DB 2; Lr
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-08-592-541-107
                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 107
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 107
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  : 198 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 800
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                                                                                                           OPERATING SYSTEM:
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U.S.A.
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-124-698-107
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COUNTRY:
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198 base pairs

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Patent No. 6210919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: PRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.3%; Score 41; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                              Query Match 1.3%; Score 41; DB 3; Length 198; Best Local Similarity 100.0%; Pred. No. 9.6e-09; Matches 41; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                             1194 ccttggcctcccaaagtgctgggattacaggcatgagccac 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-496-841C-107; Sequence 107, Application US/08496841C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107, Application US/09127480 Patent No. 6194153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: DNA (genomic) US-09-127-480-107
       ; TYPE: nucleic acid
; STRANDEDNESS: single
TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-124-698-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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Gaps
general information:
GENERAL INFORMATION:
GENERAL INFORMATION:
GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
FRASER, PAUL C
FOUNTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO _____
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APPLICANT: ST. GENER-HYSLOP, PETER H
APPLICANT: ST. GENERS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENERIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1194 ccttggcctcccaaagtgctgggattacaggcatgagccac 1234
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 CCTIGGCCTCCCAAAGIGCTGGGATTACAGGCATGAGCCAC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
APPLICATION NUMBER: US/08/496,841C
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-08-496-841C-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 753-6237
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 103, Application US/08967101 Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                              STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/967,101
FILING DATE: 10.NOV-1997
CLASSIFICATION NUMBER: 08/592,541
FILING DATE: 10.NOV-1997

APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE: Education Filing Filing Filing Filing DATE:
ATTORNEY/AGENT INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION NO: 103:
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Search completed: September 20, 2002, 06:14:47 Job time: 11106 sec us-09-846-456-1.oli.rst

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September 20, 2002, 00:17:46; Search time 3900.56 Seconds (without alignments) 11180.103 Million cell updates/sec
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3231
1 acagggcatggtggcaggtg......gccccacatccccacct 3231
                                                                                                                                                                                                                                                                                                                                                                                                                             27472414
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                             13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                    OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                Sequence:
                                                                                                                          Run on:
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1: em\_estba:\*
2: em\_esthum:\*
3: em\_esthum:\*
4: em\_estru:\*
5: em\_estro:\*
6: em\_estro:\*
7: em\_estro:\*
10: qb\_estr:\*
11: qb\_htc:\*
11: qb\_htc:\*
13: em\_gss\_inv:\*
14: em\_gss\_inv:\*
15: em\_gss\_pln:\*
16: em\_gss\_vrt:\*
17: em\_gss\_vrt:\*
18: em\_gss\_vrt:\*
18: em\_gss\_vrt:\*
19: em\_gss\_vrt:\*
10: em\_gss\_vrt:\*

and is derived by analysis of the total score distribution.
SUMMARIES

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COLUMNICO		ID	AU121731	AU135588	244377	AW748338	AA527406	BG678861	BE178833	AQ538994	AA652813	AG067644	BI059823	BI015195	BG745912	BG014649	BG007260	AQ056873	AA010265
		DB	. 6	6	10	9	σ	10	σ	12	9	12	10	10	10	10	10	12	6
		Query Match Length DB	763	736	292	289	467	866	617	219	424	674	569	009	1054	384	387	444	325
	æ	Query Match	10.4	6.7	4.8	3.9	3.4	3.0	1.8	1.8	1.8	1.8	1.7	1.7	1.7	1.7	1.7	1.7	1.7
		Score	336	217	154	126	111	86	28	57	57	57	56	56	26	55	55	55	54
		Result No.	1	7	3	C 4	S	φ	c 2	00	6	c 10	11	c 12	. 13	14	15	c 16	17

54 1.7 465 10 BF431825 54 1.7 468 9 AW104031 52 1.6 453 12 AG653862 52 1.6 58 9 A1616607 52 1.6 533 10 B1062371 52 1.6 534 10 B1062371 52 1.6 414 9 AAR81408 52 1.6 414 9 AAR81408 52 1.6 414 9 AAR81408 52 1.6 414 9 AAR81408 52 1.6 417 9 A1679952 52 1.6 417 9 A1679952 52 1.6 455 9 A1002069 52 1.6 456 9 A1002069 52 1.6 457 9 A1002069 52 1.6 457 9 A1002069 52 1.6 530 9 AA886970 52 1.6 530 9 AA886970 52 1.6 583 9 A10845933 52 1.6 583 9 A1084593 52 1.6 583 9 A1084593 52 1.6 530 9 AA886970 52 1.6 530 9 AA886970 52 1.6 530 9 AA886970 53 1.6 530 9 AA886970 51 1.6 52 330 9 AA886970 51 1.6 523 9 A06238966 6E57.  Homo sapiens Contact: Takao Isogai Genomics Laboratory Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Helix Research Institute of Medical Andrea Parent P	BF431825 nab50h08.  AN104031 xd64a05.x BG576148 602597119 AQ663862 HS_2151_B A1610607 tp19909.x B166237 11.3.4 UP011 B7710918 id94904.y B1711369 id94904.y B1711369 id94904.y A126419 q1080h11.x AA48110 2x00209.s A167942 tu63h07.x A1679952 tu67h07.x B16629824 0x22a01.x A1679952 tu67h07.x B1062368 IL3-UT011 A1089524 ox22a01.x A1002969 an23903.s AQ489571 RPCI-11-2 AW917124 EST383813 AQ623696 HS_5319_A A1084593 ox63f01.s AQ63369 HS_5319_A A1084593 ox63f01.s AQ198714 RPCII1-59 AQ198714 RPCII1-59 AQ198714 RPCII1-59 AQ486570 ab517612.r BF934753 CM1-NT020	ENTS	bp mRNA linear EST 19-OCT-2000 cDNA clone MAMMA1000851 5', mRNA	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. ., Ishii,S., Saito,K., Kawai,Y., amura,Y., Nagai,T., Sugano,S. and	e Chiba 292-0812, Japan	3'-end one pass sequencing: Helix ary construction: Department of 1 Science, University of Tokyo, and ens" "	158 t 3 others
54 1.75 54 1.75 554 1.75 554 1.75 553 1.6 553 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 553 1.6 553 1.6 554 1.6 555 1.6 555 1.6 556 1.6 557 1.6 558	AMI04031 BG576148 AG576148 AIG10607 AIG10607 BI702371 BI711369 AIZ64119 AAZ679448 AAZ679448 AAZ679952 AAZ679952 AAZ679952 AAZ679952 AAZ6799533 AQ489571 AQ489570 AAZ66976 AAG67976 AAG6	ALIGNMENT	763 sapiens 966	ta; es; ki,Y Nak	st k cute 1, Chiba 2	co.jp. 6 3 55 6 3 51. 55 6 3 51. 6 4 51. 6 4 51. 6 5	or: pME185 260 g
54 1.75 54 1.75 554 1.75 554 1.75 553 1.6 553 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 552 1.6 553 1.6 553 1.6 554 1.6 555 1.6 555 1.6 556 1.6 557 1.6 558	10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		ошо	a; C a; E 3) ,T.,	ojec ) ) ogaj rry rry stit razu	rri.cojecojecojecojecojecojecojecojecojecoje	o Ç
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Gaps

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0; Indels

0; Mismatches

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Matches 217; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                3016 tttgctccttgtttttccccggttctgttttctcccttctccggaaggcttgtcaagg 3075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases I to 736)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TIGCICCTIGITITITICCCCGGITCIGITITICTCCCCTICTCCCGAAGGCITGTAGG 180
                                                                                                                                                                                                                                                                                                          241 TACTIGGGCGTTATIGTTTTGTTTCGAGGCCAAGGGCTTCGGGAAGTGCTCGGTTTCG 300
                                                                                                             1 AATTGCGAGCGAGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTCCC 60
                                                0; Gaps
     Ouery Match 10.4%; Score 336; DB 9; Length 763; Best Local Similarity 100.0%; Pred. No. 1.9e-126; Matches 336; Conservative 0; Mismatches 0; Indels
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1532-3 Yana, Kisarzau, Chiba 292-0812, Japan
TTE1: 81-438-55-3951
Fax: 81-438-52-3952
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199 c 199 g 170
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AU135588.1 GI:10996127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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Length 736;

DB 9;

6.7%; Score 217; DB 9; 1 100.0%; Pred. No. 6.9e-78;

Query Match Best Local Similarity

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/tissue_type="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

87 c 96 g 56 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ bases 1 to 292]

Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
2958 gctgcggcagggcagggcgggggggccccgcccaacagagccggttctcagggcgctt 3017
                                                                                                                                                65 GCTGCGGCAGGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSC1ZB081 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lzb08
Seq primer: ('21)M13_universal.
Location/Qualifiers
                                                                                                                            Genexpress Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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95277534
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Pred. No. 5.7e-52;
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/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                               3078 taggagaaagagacgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                           185 TAGGAGAAAGAGGCAAACACAAAAGTGGAAAACAG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.8%;
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Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL 7. This entry can be seen in the following URL 2. 271099-012-c10643-1999-10-276t4-1) Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW748338 1252-271099-012-c10 BT0252 Homo sapiens cDNA, mRNA sequence.
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1 (bases 1 to 289)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D. H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                              2910 gtgagtggggcgggacccgcagagccgaccgcgaccttctccccgggctgcggcaggg 2969
                                                                                                                                                2970 cagggcggggagctccgcgcaccaacagagccggttctcaggggcgctttgctccttgttt 3029
                                                                                                                                                                                                                                               3030 tttccccggttctgttttctccccttctccggaaggcttgtcaaggggtaggagaaagag 3089
                                                                                                                                                                                                                                                                           61 CAGGGGGGGAGCTCCGCGCACACAGAGCCGGTTCTCAGGCGCTTTGCTCTTGTTT 120
                                                                                                 1 GTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGG 60
     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
     1; Indels
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     0; Mismatches
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/db_xref="taxon:9606"
/clone_lib="BT0252"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 146
High quality sequence stop: 289.
Location/Qualifiers
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Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                   3090 acgcaaacacaaaagtggaaaacag 3114
                                                                                                                                                                                                                                                                                                                                                                                                    181 ACGCAAACACAAAAGTGGAAAACAG 205
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     Matches 204; Conservative
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS27406 467 bp mRNA linear EST 21-AUG-1997 ag37c02.sl NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:936962 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 467)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                              2006 gotgoacttcacaaatgtatacaaactaaatacaagtcotgtgtttttatcacagggagg 2065
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100.0%; Pred. No. 1.6e-34;
3.9%; Score 126; DB 9; Length 289; 100.0%; Pred. No. 1.5e-40; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image/thml
Insert Length: 1057 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 t
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/clone_lib="NCI_CGAP_Co3"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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Matches 111; Conservative
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Unpublished (1997)
                                                        Matches 126; Conservative
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AA527406
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          2126 ttgttt 2131
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DEFINITION

RESULT BG678861

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KEYWORDS

SOURCE

VERSION

ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Hqu608"
/dev_stage="Adult"
/dote="Organ: head_neck; Vector: pucl8; Site_l: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
34 a 128 c 150 g 145 t
                                                 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costo, F. F., Goldman, G.H., Carvalho, A.F., Matcukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-PMO-HT0608-170
300-001-f02&t3=2000-03-17&t4=1)
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RPCI-11-343L18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-343L18
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                             Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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High quality sequence start: 14
High quality sequence stop: 612.
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Other_GSSs: RPCI-11-343L18.TV
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                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ538994.1 GI:4869633
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                                                        REFERENCE
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COMMENT
                                                                                AUTHORS
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                                                                                                                                                                                                                                                 602624760F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749735 5',
                                                                                                                                                                                                                                     EST 01-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Bamal: capabs-remail.nih.gov.
Tissue Procurement: James Cleaver, M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10603 row: g column: 16
High quality sequence stop: 860.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
0; Gaps
                                                               2212 totgaggacctggggagctcaggctgggaatctccaaggcagtaggtcgc 2262
                                                                                            Length 998;
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/db_xref="taxon:9606"
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Matches 98; Conservative
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source

FEATURES

BASE COUNT

ORIGIN

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ACCESSION

VERSION

KEYWORDS

BE178833/c

RESULT LOCUS ORGANISM

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Gaps

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissue Procurement: W. Marston Li.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                   Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
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Insert Length: 560 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
                                                                              9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB.7631609"
/db_xref="taxon:9606"
/clone="RRCI-11-343118"
/clone_lib="RRCI-11"
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/db_xref="taxon:9606"
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Location/Qualifiers
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/ ALCOUNTY OF THE PAMPIO; Site_1: Not1; Site_2: ECORI; 1st strand CDNA was primed with oligo(dT)17 on 50 ng of burse-treated, total cellular RNA obtained from 5,000-10 DNAse-treated, total cellular RNA obtained from 5,000-10 ,000 microdissected preneoplastic cells histologically determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMPIO by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Totoki,Y., Mattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Matanabe,H. and Sakaki,Y.
Direct Submission
Submitted (O2-Aug-2001) Asao Fujiyama, The Institute of Physical
Bubmitted (O2-Aug-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG067644.1 GI:16619446
AG067644.1 GI:16619446
GSS; GSS (genome survey sequence).
GSS; GSS (genome survey sequence).
Fan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-057L02.R.
Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG067644 11near GSS 03-NOV-200:
Pan troglodytes DNA, clone: PTB-057L02.R, genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 57; DB 9; Length 424; 100.0%; Pred. No. 1.8e-12;
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/db_xref="taxon:9598"
/clone="PTB-057L02.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. nv.
/clone="IMAGE:1189352"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
                                                                                      /dev_stage="45 years old"
/lab_host="DH10B"
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R.Site 1 : SacI
R.Site 2 : SacI.
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Query Match 1.7%; Score 56; DB 10; I
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 56; Conservative 0; Mismatches 0;
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/clone_lib="ET0140"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                               BI015195.1 GI:14419266
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                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                      AUTHORS
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KEYWORDS
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                    LOCUS
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Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H.,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESD/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL3&t2=LL3-UT0115-
809 primer: puc 18 forward
High quality sequence stop: 568.
                                                                                                                                                                                                                                         EST 15-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: uterus_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from OrBSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of Lissue mRNA and cDNA amplification were performed under 11 stem mRNA and publication were performed under 11 of 11 of 119 g 161 t
                                                                                                                                                                                                                            BIO59823
IL3-UT0115-080101-378-H06 UT0115 Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homínidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simpson, A.J. \\ Shotgun sequencing of the human transcriptome with ORF expressed \\
                                                          Gaps
                                                                                     1025 ctcactgtaacctctgcctcccgggttcaagcgattctcctgcctcagcctcctgag 1081
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0
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                Length 674;
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100.0%; Pred. No. 4e-12;
tive 0; Mismatches 0; Indels
                                                      Indels
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                                 1.4e-12;
            DB 12;
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/db_xref="taxon:9606"
/clone_lib="UT0115"
/dev_stage="Adult"
                                 Pred. No.
            Score 57;
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BI059823.1 GI:14467350
        1.8%; ;
100.0%;
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                                               57; Conservative
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TITLE

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BI015195 600 bp mRNA linear EST 13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: lung_tumnor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from OrBSTES PCR (U.S. Letters Patent appplication No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=MR4&t2=MR4-ET0140-
190201-006-e12&t3=2001-02-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 72.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
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602724092T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850375 3',
mRNA sequence.
BG745912
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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High quality sequence start: 14 High quality sequence stop: 371
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/lab_host="DH10B (phage-resistant)"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCMG91 row: h column: 24
High quality sequence stop: 841.
Location/Qualifiers
                                                                                                                              1 (bases 1 to 1054)
NIH-WGC http://mgo.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Dr. Mark Watson
CDNA Library Predicin: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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100.0%; Pred. No. 2.9e-12;
tive 0; Mismatches 0; Indels
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/clone="IMAGE:4850375"
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Matches 56; Conservative
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/note—"Organ: placenta_normal; vector: puc18; Site_1: Smal
Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under ling to the puc 18 vector. 8 verse
110 c 87 g 100 t 1 others
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LL5-GN0239-271100-281-e06 GN0239 Homo sapiens CDNA, mRNA sequence.
BG007260
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matal: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
thtp://www.ludwig.org.br/scripts/gethtm12.pl?t1=IL5£t2=IL5-GN0239-
271100-281-e066t3=2000-11-278t4=1)
Seq primer: puc 18 forward
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Fax: +55-11-2704922
Fax: +55-11-2707001
Bmail: asimpson@ludig.org.br
Project: This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-GN0239-211200-342-907&t3=2000-12-21&t4=1)
Seq primer: puc IB forward
High quality sequence stop: 360.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Bulkaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(base 1 to 325)
Hillier.L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Fuller, Leny, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTyT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo."
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325 bp mRNA linear EST 09-MAY-19
Z109e05.31 Soares_fettal_liver_Spleen_INFLS_S1 Homo sapiens cDNA
clone IMAGE:430304 3' similar to contains Alu repetitive element
contains element MER22 repetitive element i, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1517 Std Error: 0.00
Seq primer: mob.REGA+FT
High quality sequence stop: 274.
                                                                                     1190 cccaccttggcctcccaaagtgctgggattacaggcatgagccactgcgcccagc 1244
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xxef="GDB:1330073"
/db_xxef="taxon:9606"
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                                          55; Conservative
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                                                                                                                                          /note="Organ: placenta_normal; Vector: pucl8; Site_1: Smal Site_2: Smal; A mini-library was made by cloning products derived from ORESTES FOR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Adams,M.D. Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Simon,M. and Venter,J.C.
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="taxon:9606"
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/sex="Male"
                                                                                                 /clone_lib="GN0239"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ncce="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Ilbraries were mixed, and ss circles were made in vitro. Following Hap purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NDHSF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-15237 Soares ND2HF8-9W pool 1: 758280-766583, 772104-774407 Soares NDHPA pool 1: 723720-726407, 739080-74099 Subtraction by Bento Soares and M. Fatima Bonaldo."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 385.
Location/Qualifiers
                                                                                                         BF431825
nab50h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3269606 3' similar to contains Alu repetitive element contains element MER22 repetitive element; mRNA sequence.
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/lab_host="DH10B"
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Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 54; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lln.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: ovary; vector: pcwv-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo draverage insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 468)
                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.e. column: 06
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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Gaps

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Contact: Robert Strausberg, Ph.D.
Email: capabbs-rémail.nih.gov
Email: capabbs-rémail.nih.gov
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
NWW-bio.llnl.gov/bbrp/image/image.html
Insert Length from Gibco
High quality sequence stop: 372
                                                                                                                                                                                                                                          AI610607
tp19909.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188288 3'
similar to TR:Q99634 Q99634 RIG-G. [1] ;contains Alu repetitive
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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IL3-UT0117-160301-502-E10_1 UT0117 Homo sapiens CDNA, mRNA
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              Pred. No. 7.5e-11; 
; Mismatches 0;
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1.6%; Score 53; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 6.2e-11;
Matches 53; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:2188288"
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BI062371.1 GI:14469898
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AI610607.1 GI:4619774
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Unpublished (1997)
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                     Best Local Similarity
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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HS_2151_B1_G10_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2151 Col=19 Row=N, DNA sequence.
                                                                                                                                                                                  /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dr primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Eax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                             /clone="IMAGE:4705901"
/clone_libe.NIH_MAC_87"
/tissue_type="nammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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100.0%; Pred. No. 2.2e-11;
tive 0; Mismatches 0; Indels
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Plate: 2151 row: N column: 19
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                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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Matches 54; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; 1 (bases 1 to 340)

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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistan, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cadenas, M., Globons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml).

(http://genome.wustl.edu/est/lambda_protocol.shtml).

please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Human insulinoma"
/tissue_type="insulinoma"
/lab_host="HH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_l:
XhoI; Site_2: ECORI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                   Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 190.
                                                                                                                                                             Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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                                                                                                             Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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100.0%; Pred. No. 2.6e-10;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@blobp.harvard.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0117-
160301-502-El0_1&t3=2001-03-16&t4=1)
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 233)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please confact Hiroshi Inoue, MD/Phb for further
Information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
                                                                                                                                                                                Library was constructed by Dr. J. Ferrer In vivo mass-excised to Bheuseript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For Information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Sossible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 316.
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/tissue_type="insulinoma"
/labot="Dype="insulinoma"
/labot="Dype="insulinoma"
/labot="Dype="insulinoma"
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XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
//inversity protocol
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                 Endocrine Pañcreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/db_xref="taxon:9606"
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/lab_host="DH10B"
//note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/Dbrpy/lmage/image.html
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop:
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M. (bases 1 to 414)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
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100.0%; Pred. No. ...
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/clone="IMAGE:746368"
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Best Local Similarity 100.0
Matches 52; Conservative
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δλ
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.,
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M. A.G.E. Consortium/LLNL at:
www-bio.linl.gov/bbrp/image/image.html
Insert Length: 1074 Std Error: 0.00
                                                           ]. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 416)
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416 bp mRNA linear EST 15-DEC-19
tu63h07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2255773 3'
similar to contains Alu repetitive element; contains element TAR1
repetitive element; mRNA sequence.
A1679442
A1679442.1 GI:4889624
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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100.0%; Pred. No. 2e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             1.6%; Score 52; DB 9; Length 414;
100.0%; Pred. No. 2e-10;
tive 0; Mismatches 0; Indels
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High quality sequence stop: 400.
Location/Qualifiers
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Matches 52; Conservative
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
sert Length: 528 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop:
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                   AI337065 417 bp mRNA linear EST 15-FEB-1' qx82q11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009060 3' similar to contains Alu repetitive element;, mRNA sequence.
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Score 52; DB 9; Length 417;
Pred. No. 2e-10;
0; Mismatches 0; Indels
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/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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Best Local Similarity 100.0%; Pred. No. 2e-Matches 52; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
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AI679952.1 GI:4890134
                                                                                                                                                                                                                                                                                                                                               AI337065.1 GI:4073992
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VERSION

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Gaps

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Best Local Similarity 100. Matches 52; Conservative

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Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=Li3st2=ILi3-UF0117-
160301-502-610st3-2001-03-16st4=1)
Seq primer: puc 18 forward
High quality sequence stop: 450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A min1.11brary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 01-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIO89524 455 bp mRNA linear EST 01-OCT-1998 oz22a01.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676040 3' similar to contains Alu repetitive element;, mRNA
                     Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Consortium (info@image.llnl.gov) for further information.
Insert Length: 761 info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 444.
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/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone_lib="UT0117"
/dev_stage="Adult"
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                                                                    Tel: +55-11-2704922
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Best Local Similarity
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq Primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 450)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunsreain,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsreain,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Bmall: Gapbs-r@mall.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/do_xef="texon:9606"
/clone="IMAGE:2556157"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
/lab_host="full features"
                                                                                                                         1 (bases I to 417)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 417;
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Ludwig Institute for Cancer Research
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Location/Qualifiers
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                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
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KEYWORDS
SOURCE
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                                        Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 105 c 111 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 09-JUN-1998
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 484)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,

White, Y., Wylle, T., Waterston, R. and Wilson, R., Theising, B.,

Washl, NCI human EST Project
                                                                                                                                                                                                                                                                                                               ö
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 448.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1002969 MRNA linear EST 09-Janan33903.1 Gessler Wilms tumor Homo saptens cDNA clone IMAGE:109540 3' similar to contains Alu repetitive element contains element MER22 repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                             1.6%; Score 52; DB 9; Length 455; 100.0%; Pred. No. 1.9e-10; tive 0; Mismatches 0; Indels
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/clone="IMAGE:1699540"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                  52; Conservative
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VERSION
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ORIGIN

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                                                                                                                                                                                                                                            AQ489571 GSS 24-APR-1999
RPCI-11-230P5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-230P5,
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EST383813 MAGE resequences, MAGL Homo sapiens CDNA, mRNA sequence.
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@tesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                      Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Other GSSs: RPCI-11-230PS.TJ
Other GSSs: RPCI-11-230PS.TJ
Other GSSs: RPCI-11-230PS.TJ
Other GSSs: RPCI-11-230PS.TJ
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
Fax: 301 838 0208
Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                              0; Indels
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1.6%; Score 52; DB 9; L
100.0%; Pred. No. 1.9e-10;
Live 0; Mismatches 0;
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/note="Vector: pBACe3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:7588300"
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/clone="RPCI-11-230P5"
/clone_lib="RPCI-11"
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AW971724.1 GI:8161570
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AQ489571.1 GI:4675445
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                       Best Local Similarity 100.0
Matches 52; Conservative
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Matches 52; Conserv
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                                                Class: BAC ends
                    Seg primer: T7
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                                                                                                                                                         1 (bases 1 to 530)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                             Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Fax: (206) 616-3618

Fax: (206) 616-3887

Fax: (206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ623696 545 bp DNA linear GSS 16-JUN-HS_5319_A2_C10_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=895 Col=20 Row=E, DNA sequence.
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1 (bases 1 to 545)
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 52; DB 9; Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
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/note="Vector: pBluescriptSKm"
139 c 111 g 145 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: johnq@tigr.org
Plate: 294
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eoc RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus NbHPU, and fetal heart NbHH19W) were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization teaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools of 5000 clones made from the same 3 libraries. The pools 340488-345479, and 484488-489479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 583)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1661017"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length.470 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 CCTTGGCCTCCCAAAGTGCTGGATTACAGGCATGAGCCACTGCGCCCAGCT 400
                                                                                                                                                                              /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6%; Score 52; DB 12; Length 545;
100.0%; Pred. No. 1.7e-10;
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                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=895 Col=20 Row=E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.0%; Pred. No. 1...
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/organism="Homo sapiens"
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High quality sequence stop: 545.
Location/Qualifiers
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/lab_host="DH10B"
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Query Match

Matches

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RESULT 38 AQ589333/c DEFINITION

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

ACCESSION VERSION KEYWORDS

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AQ198714 171 bp DNA linear GSS 20-APR-1999 RPCII1-59J23,TJ RPCI-11 Homo sapiens genomic clone RPCI-11-59J23, DNA sequence.
            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 783)
Xiao, H., Peng, Y., Song, H., Gu, Y., Yang, Y., Gao, G., Xu, X., Li, N.,
Olan, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Chen, Z. and Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 171)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,B., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC. End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
thtp://www.tigr.org/tdb/humgen/bac_end_search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilBl" 186 c 182 g 171 t
                                                                                                                                                                             Homo sapiens cDNA FHTB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 753;
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
712: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                    Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="FHTBABH02"
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/lab_host="BM25.8"
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AQ198714.1 GI:3610913
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                                                                                                                                                                                                                                                                                                                                           AQ589333 717 bp DNA linear GSS 07-JUN-1999 CITBI-E1-2645K6.TF CITBI-E1 Homo sapiens genomic clone 2645K6, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV718287 FHTB Homo sapiens cDNA clone FHTBABH02 5', mRNA sequence. AV718287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
1 175 c 140 g 180 t
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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1.6%; Score 52; DB 12; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                       Length 583;
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                         1.6%; Score 52; DB 9; L. 100.0%; Pred. No. 1.7e-10; tive 0; Mismatches 0;
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/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
/sex="male"
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                                                                                                                            52; Conservative
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FEATURES

BASE COUNT

DEFINITION AV718287/C

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ACCESSION VERSION

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RESULT 39

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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kirzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylle, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ac52b01.sl Stratagene fetal retina 937202 Homo sapiens CDNA clone
IMAGE:866185 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 216.
Location/Qualifiers
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                       Score 51; DB 12; Length 171;
Pred. No. 8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:866185"
/clone=lib="Stratagene fetal retina 937202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
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Best Local Similarity 100.0%; Pred. No. 6.9e-10
Matches 51; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                 Query Match 1.6%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 8e-Matches 51; Conservative 0; Mismatches
/organism="Homo sapiens"
/db_xref="GDB.752510"
/db_xref="taxon:9606"
/clone="RPCI-11-5923"
/clone_lib="RPCI-11"
                                                                                                          /cell_type="Lymphocytes" /note="Vector: pBACe3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                         232 bp
                                                                                                                                                                      44 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAĞ62976
AAĞ62976.1 GI:2616967
                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                    32 c
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Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
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1 (bases 1 to 30)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashUr Werck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
Insert Size: 1095
High quality sequence stops: 320
Source: IMAGE Consortium, Linl.
This clone is available royalty-free through Linl.; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1095 std Brror: 0.00
Seq primer: Promega -21ml3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
Length 360;
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1.6%; Score 51; DB 10; I
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 51; Conservative 0; Mismatches 0;
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/db_xref="GDB:3789342"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 320.
Location/Qualifiers
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H90008.1 GI:1080438
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RESULT 43

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Gaps

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Indels

6.9e-10; hes 0;

Bes. Matches

DEFINITION

ACCESSION VERSION KEYWORDS

AA486970/c

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ280600.1 GI:3906419
                                                                                                                                                                                                                                                     rel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence.
                                                                         sequence tags
                              Simpson, A.J.
                                                                                                                   20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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1 (bases 1 to 375)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF924753 375 bp mRNA linear EST 19-JAN-2001
CM1-NT0209-281100-609-c10 NT0209 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.

I (bases 1 to 369)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Unpublished (1997)
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                              EST 06-MAR-1998
                                                   abl/fi2.rl Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841103 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert.Length: 2381 Std Error: 0.00
Seg primer: -26m13 rev1 ET from Amersham
High quality sequence stop: 361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="texon:9606"
/db_xref="texon:9606"
/clone=lib="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72_years"
/lab_host="SOLR_cells (kanamycin resistant)"
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                                 linear
                                 mRNA
                                 369 bp
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BF924753/c
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BASE COUNT ORIGIN

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/db_xref="taxon: 3606"
/clone_lib="NT0209"
/clone_lib="NT0209"
/clone_lib="NT0209"
/note="Organ: nervous_tumor; Vector: puc18; Site_l: Smal;
/note="Organ: nervous_tumor; Vector: puc18; Site_l: Smal;
Site_l: Smal; A mini-library was made by cloning products
Garived from ORESTES PCR (U.S. Letters Patent application
NO. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Seq primer: puc 18 forward: 15
High quality sequence start: 15
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 379)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Liaboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ280600 379 bp DNA linear GSS 22-NOV-1 CITBI-E1-2516H22.TR CITBI-E1 HOMO Sapiens genomic clone 2516H22,
Shotgun sequencing of the human transcriptome with ORF expressed
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Other_GSSs: CITBL-B1-2516H22.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
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Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page
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AX239607 Sequence
AC006326 Homo sapi
AL583882 Human DNA
AF779296 Homo sapi
AC036144 Homo sapi
AL158043 Human DNA
AL163512 Mouse DNA
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AX127831 Sequence
AX138818 Sequence
AX024328 Homo sapi
AX092841 Sequence
AX092841 Sequence
AX092841 Sequence
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Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P.,
Rosier-Montus, M.F., Remaley, A. and Santamarina-Fojo, S.
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 2 08-Nov-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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AXO60721 Sequence
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AXO60890 Sequence
AXO60800 Sequence
AXO60800 Sequence
AXI37764 Sequence
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AXI37875 Sequence
AXI37873 Sequence
AXI37830 Sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2 from Patent WOO183746.
AX351030.
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AF258623S2
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                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 (bases I to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
                                                                                                                              121 ccctgctgtcagctctggccgctgccttccagggctcccgagccacacgctgggcgtgct 180
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                                        181 ggctgagggaacatggcatgttggcctcagctgaggttgctgctgtggaagaacctcact 240
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                                                                 1 tggaggtctcagctgagagggctggattagcagtcctcattggtgtgtatggctttgcagca 60
                                                                                     Direct Submission
Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Length 357;
                                         Indels
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AF275948
    100.0%; Score 357; DB 6; L 100.0%; Pred. No. 3.3e-197;
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REKLAAABERVLRSNMDILKFILNSTSPFPSKELABATKTLIHSLGTLAGELFSNR
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GROFTEEDEAFEYDNSTTPEYCNDLMRTLESSPIETIIWKALERLLVGKTLITTPDTPAT
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Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P.,
Rosier-Montus, M.F., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 5 08-NOV-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.9e-137;
0; Mismatches 2;
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47 c 48 q 32
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Query Match 44.5%; Score 159; DB 6; Length 159; Best Local Similarity 100.0%; Pred. No. 2e-81; Matches 159; Conservative 0; Mismatches 0; Indels

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (07-JAN-2000) Porsch-Oezcueruemez M.K., Institute for
Clinical Chemistry, University of Regensburg,
Franz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
100 ttaatgaccagggggggtccctgctgtcagctctggccgctgccttccagggctccc 159
                                                                  160 gagccacacgctgggcgtgctggctgagggaacatggcatgttggcctcagctgaggttg 219
                                                                                   Porsch-Oezcueruemez, M., Langmann, T. and Schmitz, G. Cloning and Characterization of the human ATP-binding Cassette Transporter-1 (ABC-1) Promoter
                   199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagaagacaaaca 258
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/function="cholesterol efflux regulatory proteiin"
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                                                                                                                                                                                                                                                        HSA252277 480 bp DNA linear PRI (Homo sapiens partial ABC-1 gene for ATP-binding cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ATP-binding cassette transporter-1"
/protein_id="CAC21428.1"
/db_xref="G1:12140345"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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189. .346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/chromosome="9"
/map="9931"
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                                                                                                                                                                                                                                                                                        transporter-1, exon 2.
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Matches 159;
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United: Submission.

Submisted (01-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, Cabonited (01-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk

On Jun 8, 2001 this sequence version replaced gi:14272260.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with an all overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw., SWISSPROT; Tr., TREMBL; WP., Vorman on the MORMPEP http. Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorman earner as the Vorm
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                                                                                                                                                                                                                                                                                                                                                                       AL353685 129608 bp DNA linear PRI 01-JUN-200:
Human DNA sequence from clone RP11-31J20 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/Chr9
RP11-31J20 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone RP11-31J20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-31J20 is at 129608 in this sequence. The true right end of clone RP11-413C10 is at 2000 in
347 GTAAGCTIGGGTITITCAGCAGCGGGGGTTCTCTCATTITITCTTGTGGTTTTGAGTT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1358. 1653
/note="Alucc repeat: matches 1. .288 of consensus"
/note="L2 repeat: matches 2649. .2698 of consensus"
2496. .2714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .250 of consensus"
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                                                                                                                             319 ggggattggaggaggagggaggaaggaagctgtgttg 357
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VECTOR: pBACe3.6
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1. .129608
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Direct Submission
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AL353685/c
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/note="LiMD2 repeat: matches 5774. .6331 of consensus" 40256. 40534 //note="L2 repeat: matches 2256. .2533 of consensus" 41476. .41615 Anote="Alusy repeat: matches 7. .302 of consensus" 22320. .22439
Anote="Min repeat: matches 10. .146 of consensus" 25533. .22839
Anote="Alusx repeat: matches 1. .307 of consensus" 2347. .23945
Anote="L2 repeat: matches 2137. .2750 of consensus" 24245. .2454
Anote="Alusy repeat: matches 2. .302 of consensus" 24565. .2454
Anote="Alusy repeat: matches 2. .302 of consensus" 24566. .24587
Anote="Bootes 4 mer acac 96% conserved" 26504. .26561 3237. .3415
/note="Limb repeat: matches 5696. .5821 of consensus"
/note="Limb repeat: matches 1. .295 of consensus"
/note="Limb repeat: matches 6040. .6173 of consensus"
/note="Limb repeat: matches 6040. .6173 of consensus"
/note="Alusc repeat: matches 1. .298 of consensus" // note="12" repeat: matches 2611. .2701 of consensus" 15380 ..15411 // note="16 copies 2 mer ac 87% conserved" 16105. .16144 // note="10 copies 4 mer caca 100% conserved" 16868 ..17049 // note="Missage 1.7049 ... matches 64. .246 of consensus" // note="Alusg repeat: matches 1. .287 of consensus" // note="Alusg repeat: matches 1. .293 of consensus" 18259. .18533 // note="Alusg repeat: matches 1. .293 of consensus" 2010. .20616 // note="Alusg repeat: matches 1. .308 of consensus" 20957 ... 21107 73293. .33380 70cte="MEREA repeat: matches 14. .106 of consensus" 70cte="22 copies 4 mer atgg 79% conserved" 70cte="14588" 70cte="MEREA repeat: matches 13. .189 of consensus" 70cte="MIR repeat: matches 49. .198 of consensus" 5802. .33591 /note="MER5A repeat: matches 60. .188 of consensus" 32450. .32536 /note="L2 repeat: matches 1363. .1940 of consensus" 13890. .13969 /note="AluSp repeat: matches 1. .308 of consensus" 31987. .32116 note="Alusc repeat: matches 1. .308 of consensus" 39674. .40243 /note="Alusq repeat: matches 1. .302 of consensus" 31424. .31734 7.00ce"11 copies 4 mer tata 81% conserved" 27998. .28103 7.00ce"MIR repeat: matches 28. .145 of consensus" 28515. .28626 7.00ce"MIR repeat: matches 17. .129 of consensus" 28986. .29213 7.00ce"MIR repeat: matches 2. .245 of consensus" 30121. .30422 //note="MIR repeat: matches 49. .212 of consensus" 21783. .22078 /note="MIR repeat: matches 77. .248 of consensus" 37183. .37260 "29 copies 2 mer ta 69% conserved"
16849. .26892 //note="2 copies 39 mer 92% conserved"
37673. .37980 .12713 repeat\_region

/note="Ally repeat: matches 5. .298 of consensus"
56027. 56232
/note="Ally repeat: matches 21. .259 of consensus"
56233. .56286
/note="18 copies 3 mer tgt 72% conserved"
56342. .56673
/note="LiMA9 repeat: matches 5893. .6307 of consensus"
56750. .56899
/note="LiMA9 repeat: matches 2565. .2710 of consensus"
57406. .57567
/note="MERSA repeat: matches 4. .187 of consensus"
57864. .58174
/note="Allosg repeat: matches 1. .311 of consensus"
59443. .60004 /note="Alugh repeat: matches 3. 311 of consensus" 50189. 50347 / note="Alugh repeat: matches 5. 155 of consensus" 51677. 51977 . 51977 / note="Alugh repeat: matches 1. 303 of consensus" 52025. 52123 / note="L2 repeat: matches 1655. 1753 of consensus" 54025. 5213 / note="MIR repeat: matches 25. 246 of consensus" 54754. 55032 / note="Alugh repeat: matches 25. 246 of consensus" 54754. 55032 / note="Alugh repeat: matches 1. 302 of consensus" 55042. 55343 /note="AluSq repeat: matches 145. .313 of consensus" 49097. .49181 /note="L2 repeat: matches 2625. .2710 of consensus" 49578. .49758 /note="Alusx repeat: matches 1. .299 of consensus" 65342. .65441
/note="MER54A repeat: matches 72. .186 of consensus" 6825. .67131 /note="L2 repeat: matches 2088. .2723 of consensus" 60201. .60355 /note="16 copies 4 mer atat 68% conserved" 64981. 65042 Anote="MERSA repeat: matches 15. .72 of consensus" 65043. 65341 /note="LTR16A repeat: matches 6. .450 of consensus" 45359. .45486 /note="AluSx repeat: matches 1. .306 of consensus" /note="MIR repeat: matches 1. .139 of consensus"
46654. .46693
/note="10 copies 4 mer acac 97% conserved"
47118. .47429
47915. .48083 /note="MIR repeat: matches 20. .183 of consensus" 63991. .64159
/note="MIR repeat: matches 78. .243 of consensus" 64590 .64653
/note="32 copies 2 mer ta 70% conserved" 64593 .64656 /note="MIR repeat: matches 155. .182 of consensus" 49874. .50188 /note="MIR repeat: matches 30. .185 of consensus" 42010. .42194 //note="MIR repeat: matches 49. .234 of consensus" 44809. .45239 /note="MIR repeat: matches 9. .188 of consensus" 49847. .49873 repeat\_region

Ouery Match 44.5%; Score 159; DB 9; Length 129608; Best Local Similarity 100.0%; Pred. No. 2.7e-81; Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT

SOURCE

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Sirrien, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A. Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Darellano, K., Dowarr, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gago, D., Galagan, J., Gardfyns, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Meeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Meeler, J., Wu, X., Direct Subnission
                                                                                                                                                                                                                                                                                                                 HTG 22-APR-2000
                                                                                                                                                                                                                                                                                                       AC012230 175064 bp DNA linear HTG 22-APR-2000
Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-02T-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 22, 2000 this sequence version replaced gi:6454033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; agarose-fp
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                     Web site: http://www-seq.wi.mit.edu
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Center clone name: 1_M_10
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Homo sapiens, clone RP11-1M10
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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03 103016: contig of 5015 bp in length 107 103116; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 
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f 1270 bp in length
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9686: contig of 1107 bp in length
9786: gap of 100 bp
12253: contig of 2467 bp in length
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12354 15228: contig of 2875 bp in length
15229 15328: gap of 100 bp
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6433: contig of 4676 bp in length
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71458: contig of 2921 bp in length
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Lono sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1) and SNAP protein genes, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183999)
gtaagettgggtttttcagcagcggggggttctctcattttttttgtggttttgagtt 318
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2010, Y., Cavelier, L., Chiu, S., Yang, X., Rubin, E. and Cheng, J.F. Human and mouse abcel comparative sequencing and transgenesis studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
                                                                                                                                                                                                                                                                                                                                      Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceride levels Patent: WO 0115676-A 1 08-MAR-2001; University of British Columbia (CA); Xenon Genetics Inc. (CA) Location/Qualifiers
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Submitted (13-JUL-2000) Genome Science Department, Lawrence
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/db_xref="taxon:9606"
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Sequence 1 from Patent W00115676.
AX092589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 175064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
          138160 145491: contig of 7332 bp in length 145492 145591: gap of 100 bp 145592 157391: contig of 11800 bp in length 157392 157491: gap of 100 bp 157492 175064: contig of 17573 bp in length.
                                                                                                                                                    /clone="RP11-1M10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.5%; Score 159; DB 2; L Lilarity 100.0%; Pred. No. 2.7e-81; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31439. 34299

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Matches 159; Conserv
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TITLE JOURNAL

AUTHORS

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FEATURES

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KLEPTATEWALINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERL
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Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
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136959. .13
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141340. .14
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
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1 (bases 1 to 90698)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, Conne RP11-24J9

Unpublished
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Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
AC021345
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100.0%; Pred. No. z...
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145441. .145513
/gene="ABCA1"
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/gene="ABCA1"
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/number=31
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/gene="ABCA1"
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148527. .148575
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148771. .14
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Best Local Similarity 100.
Matches 159; Conservative
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Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Olonson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McKernan, K., McMernan, C., Moldrim, J., Meneus, L., Morrow, J., Naylor, J., Norrow, J., Norrow, J., Norrow, J., Norrow, J., Norrow, J., Naylor, J., Pierre, N., Pisani, C., Polnard, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Lircell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Lircell, Jan. 2000 Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

No Jul 13, 2000 this sequence version replaced gi:6705761.

All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu ------ Project Information Center project name: L4483
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12840 13710: cont
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5759: cor
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Direct Submission
Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
Sequence update by submitter
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10442)
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Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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/db_xref="taxon:9606"
. 2297 c 2408 g 2835
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Sequence 1 from Patent WO0078972.
AX060713
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Best Local Similarity 99.29
Matches 127; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABC1 gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
promoter region, and four polymorphisms
2 (bases 1 to 200)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Rosier-Montus,M.F., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 8 08-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 2.4e-46;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
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/db_xref="GI:9755159"
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                                                         /codon_start=1
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            /gene="ABCA1"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Schwartz, K., Lawn, R.M. and Wade, D.P.
ABCAl gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR
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AF285167
                                                                                                                                                                 1 (bases 1 to 10442)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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Lawn, W., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Direct Submission
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                            Sequence 1 from Patent WO0078971.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/chromosome="9"
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/tissue_type="skin"
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ARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
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SWSDMRQEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
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KLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT
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KSYVSSTNLPVLALLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVA
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RILDGGGQNDILEIKELTKIYRRRRPAVDRICVGIPPGECFGLLGVNGAGKSSTFKM
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PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARI
FSILSQSKKRLHIEDYSVSGTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT
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/product="ATP-binding cassette transporter 1"
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99.2%; Pred. No. 2.2e-33;
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AX060719.1 GI:12406108

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10474)
                                                                                                                                                                                         Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10474)
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Tarp binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
                                                                                                                                                                                                                                                   Lawn, R.M., Wade, D., Óram, J.F. and Garvin, M.
Atp binding cassette transporter protein abcl polypeptides
Patent: WO 0078971-A 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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21.6%; Score 77; DB 6; Length 10474;
Best Local Similarity 99.2%; Pred. No. 2.2e-33;
Matches 127; Conservative 0; Mismatches 1; Indels (
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/db_xref="taxon:9606"
2304 c 2415 g 2844
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Sequence 7 from Patent WO0078971.
AX060898
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I bases 1 to 10474)

Lawn, R.M., Wade, D. and Garvin, M.

Regulation with binding cassette transporter protein abcl Patent: Wo 0078972-A 9 28-DEC-2000;

CV THERAPEDICS, INC. (US)
                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I bases 1 to 10474)

Lawn, R.M., Wade, D. and Garvin, M.

Regulation with binding cassette transporter protein abcl Patent: Wo 0078972-A 7 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
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99.2%; Pred. No. 2.2e-33;
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                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     131 agetetggcegetgcettecagggetecegagecacacgetgggegtgetggetgaggga 190
              Gaps
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Zhao.L.X., Zhou.C.J. Tanaka.A., Nakata.M., Hirabayashi.T.,
Amachi.T., Shioda.S., Ueda.K. and Inagaki.N.
Cloning, characterization and tissue distribution of the rat
ATP-binding cassette (ABC) transporter ABCZ/ABCA2
Blochem. J. 350 (Pt 3), 865-872 (2000)
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hes 0;
                                                                                                                                                                                                           Homo sapiens mRNA for ABC1, partial cds. AB037924
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100.0%; Pred. No. 1.7
:ive 0; Mismatches
                                                                                                                                                                                                                                                                              Homo sapiens placenta cDNA to mRNA.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="placenta"
88. .298
                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 298)
Ueda,K., Kioka,N. and Tanaka,A.
Direct Submission
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88. .>298
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Matches 60; Conserv
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                                                                                                                                      381 GACAAACA 388
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PAT 15-MAY-2001

linear

DNA

Sequence 3 from Patent WO0130848.

DEFINITION

AX127764

ACCESSION VERSION

AX127764.1 GI:14134411

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Homo sapiens ATP binding cassette transporter 1 (ABCA1) mRNA,
partial cds.
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synthetic construct.
synthetic construct
artificial sequence.

[ (bases) to 446)
   Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Patent: WO 0130848-A 3 03-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    artificial sequence.

1 (bases 1 to 446)

Denefie, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searfoss Iii, G.H., Remaley, A., Brewer, H.B. and Dean, M.

Nucleics acids of the human abcl gene and their therapeutic and diagnostic application
Patent: EP 1096012-A 3 02-MAY-2001;
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1 Similarity 100.0%; Pred. No. 1.7e-23;
60; Conservative 0; Mismatches 0;
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/db_xref="taxon:32630"
/note="Oligonucleotide Primer"
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/note="Oligonucleotide Primer"
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100.0%; Pred. No. 1...
'... 0; Mismatches
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Sequence 3 from Patent EP1096012.
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Location/Qualifiers
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Location/Qualifiers
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Direct Submission
Submitted (20-FEB-2001) Kazumitsu Ueda, Kyoto University Graduate
School, Applied Life Sciences; Kitashirakawa, Kyoto Sakyo-ku, Kyoto
606-8502, Japan (E-mail:uedak@kais.kyoto-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="AIP binding cassette transporter 1"
/product="AIP binding cassette transporter 1"
/protein_id="AaF69513.1"
/db_xref="G1:7769708"
/tanslation="MACWPQUELLEWKNLTFRRQTCQLLLEVAWPLFIFLILISVRL
/translation="MACWPAPSGTLEWWYQIICNANNPCFRYPTPGEABGVVGNFNKS"
198 c 190 g 156 t 1 others
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                                                                                                                                                                                                                                                                                              Submitted (19-APR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A new topological model of functional human ABCA1-Signal peptide
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                                                                                            1 (bases 1 to 697)
Pullinger.C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
Analysis of hABCI gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Blochem. Blophys. Res. Commun. 271 (2000) In press
2 (bases 1 to 697)
Pullinger.C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
Aouizerat,B.E., Fielding,C.J. and Kane,J.P.
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HOMO Sapiens mRNA for ABCAl, complete cds.
AB055982
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100.0%; Pred. No. 1.7e-23;
iive 0; Mismatches 0;
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1. .>697
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/gene="ABCA1"
/note="membrane-bound"
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AUGGADINYEGO TERAGHKOAGKTTTMS LITGLEPPESGTAY IGKDIREEMSTIR
QULGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEOMALDVGLPSSKLKSKT
SQLSGGWRKLSVALARVGGSKYVILDEPTAGVDPYSRRGTRELLKYRQRFTILST
HHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTUVKDVPSSSLSSRNS
STVSYLKKEDSYSQSSSDAGLGSDHESDTTTDVSALSNLTRHVSBARLVEDIGHEL
TYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETS
DGTLPARRNRARGDRQSCLRPFTEDDAADPNDSDIDPESRFTDLLSGNDGKGSYQVK
GWKLTQQCFVALLWKRLLIARRSKGFFAQIVLPAAVVCIALVFSILVPPFCKTPSLE
LQPWMYNBQYTPVSNDARDTGTLELNALTKDPGFGTRCMEGNPIPDTPCQAGEEEW
TTAAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKRLDVCPPGAGGLEPPPROKNTA
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PCYVDDIFLERVWSRSMPLFWILAMIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILM
PCYVDDIFLERVWSRSMPLFWILCAMIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILM
FSWFISSLIPLIJVSAGLIVVIIKAGNILPYSDPSVYPYFLSFSPRAVYTIQCFLISTLE
SRANIAAAAGGGIIYFTLYLPYVICCAWODYVGFTKIFTRFAFAFFGFGCEYFALFE
EQGIGVQWDNLFESPYPEDGFNILTSVSWMLEDTFLKGVMTWYIEAVFFGQCGYFRLFE
TFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEFTHLKLGVSIQNLVKVYRDGMKV
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DALKOMKHIKLAKDSSADETBALGREWETGLINTNNNVWYWRNKGWHAISSFLINVIN
NAILRANLONGENPEHYGITARNIFLNALTGOLSEVALATTSVDVILVSICVIFAMSFV
PASSYVYELIOERVSKAKHLOFISGVKPVIYWLSNFVWDMCNYVVPATLVIIFICFQO
KRYVSENLIPPYLALLLLLYGWSITPHAPASSFYKETBSGTAVVTLTSVNLGIGNSVA
KRYVESTRIPPYLALLLILGWSITPHENTENTARASKYVTLTSVNLGIGNSVA
PRYLEELTDNKLNNINDILKSYFLIFPHFCLGRGLIDWYKNOAMADALERFGENRFYS
PLSWDLVGRNLFAMAVEGVYFFLITVLIQYRFIRFPRPVNAKLSPLNDEDEDVRREER
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARI
FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT
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RQYMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE
QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN
KLEPIATEVNLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT
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SWSDMRQEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDLNYKALF
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Tel:81-75-753-6105, Fax:81-75-753-6104)
Location/Qualifiers
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Sequence 3 from Patent WO0170810.
AX253452.
AX253452.1 GI:16073979
                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB63210.1"
/db_xref="GI:15212107"
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1 (bases 1 to 7862)
Attie-A.D., Cook.M., Gray-Keller,M.P., Hayden,M.R., Pimstone,S. and Brooks-Wilson,A.
Abcl modulation for the modulation of cholesterol transport Patent: WO 013184-A.1 10-MAY-2001,
WISCONSIN ALUMNI RESERREL FOUNDATION (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9741)
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Ili,G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 9741)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemonine, C., Duverger, N., Jaye, M., Searfoss, G. H., Remaley, A., Brewer, H. B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
                                                                                                                                                                                                                                                                                                                         0; Gaps
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Patent: WO 0130848-A 69 03-MAY-2001;
Aventis Pharma S.A. (FR)
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/db_xref="taxon:9606"
a 2180 c 2290 g 2620
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1861 c 2010 q
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                                                                                                              FEATURES
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 7260)
Schmitz,G. and Bodzioch,M.
Atp binding cassette transporter 1 (abc1) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid, cardiovascular or inflammatory disorders
Patent: WO 0170810-A 3 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
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1 (bases 1 to 7860)

Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and rigilyceride levels

Patent: WO 0115676-A 6 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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+'ve 0; Mismatches
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/db_xref="taxon:9606"
1765 c 1905 g 1756
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AX092594
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/db_xref="taxon:9606"
1 1860 c 2008 g 1978
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Sequence 1 from Patent W00132184.
AX135712
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                  Homo sapiens
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Matches 60; Conserv
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Patent: WO 0130848-A 70 03-MAY-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9654)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abcl gene Patent: WO 0183746-A 10 08-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      Remaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human abcl gene and their therapeutic and diagnostic application
Patent: EP 1096012-A 69 02-MAY-2001;
Aventis Pharma S.A. (FR)
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100.0%; Pred. No. 1.9e-23;
Live 0; Mismatches 0;
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Sequence 10 from Patent W00183746.
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Location/Qualifiers
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AKO24328 1556 bp mRNA linear PRI 29-SEP-2000 Homo sapiens cDNA FLJ14266 fis, clone PLACE1002437, highly similar to ATP-BINDING CASSETTE TRANSPORTER 1.
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1 (soqai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 9854)

Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C., Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss Iii,G.H., Remaley,A., Brewer,H.B. and Dean,M.

Nucleics acids of the human abc1 gene and their therapeutic and diagnostic application
Patent: Ep 109612-A 70 02-MAY-2001;
Aventis Pharma S.A. (FR)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1002437.
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16.8%; Score 60; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.9e-23;
Matches 60; Conservative 0; Mismatches 0;
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Sequence 70 from Patent EP1096012.
AX139818
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/db_xref="taxon:9606"
a 2219 c 2334 g 2635
                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
a 2219 c 2334 g 2639
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Location/Qualifiers
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AK024328.1 GI:10436685
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Matches 60; Conservative
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Submitted (23-A0G-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@thri.co.jp, Tel:81-438-52-3951, Fas:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Bhoteconology; cDNA library construction, 5'-6'-8'-and one pass sequencing and clone selection: etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /proteil_id="Bab14887.1"
/db_xref="G1:10436686"
/translatio="MacWPQLRLLLWKNLTFRRQTCQLLLEVAWPLFIFLILISVRL
SYPPYEQHECHPPNAAPSAGTLPWVGGIICNANNPCFRYPTPGEAPGVGNFNKSIV
NLSLPKSTVDKMLRADYLHKYPLQSYQLHTGLOSKSENLKLQDFLVDNETFSGFLYH
NLSLPKSTVDKMLRADYLHKYPLQSYQLHTGLOSKSEEWIOLGDOEVSELGCLP
KRKLAAARRVLKSNNDTLKPTLMDVACDDIAHGQLTVPRSAAVAATGDAKPNMMGRET
LLSICASVPKVEFHERHILEHFSFCVCVSVSLFPARGIVSFSWASFRIWVLWKAVFWQ
HGSSMAWWEGQLGLGIAIAFEYFTSIDVG"
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Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A. NEDO human cDNa sequencing project Unpublished (2000)
2 (bases 1 to 1556)
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Hayden M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.
Gompositions and methods for modulating hdl cholesterol and
triglyceride levels
Patent: WO 0115676-A 255 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
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14.3%; Score 51; DB 9; Length 1556;
Best Local Similarity 100.0%; Pred. No. 3.3e-18;
Matches 51; Conservative 0; Mismatches 0; Indels
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/tissue_type="placenta"
/clone_lib="PLACE1"
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/note="Synthetic Primer"
17 c 11 g 5
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                                                                                           Isogai, T. and Otsuki, T. Direct Submission
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Backlen, P., Enten, B., Erown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dayar, S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand - Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Lilev, T., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, K., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, C., Norbu, C., Norbu, C.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.
Hayden, M.R., and methods for modulating hdl cholesterol and
triglyceride levels
Patent: WO 0115676-A 253 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-353G1
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
                                    6.3e-09;
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/db_xref="taxon:32630"
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              9.8%; Score 35; DB 100.0%; Pred. No. 6.3 tive 0; Mismatches
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Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribey, R., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Scaman, S., Schupback, R., Scaman, S., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wilk, Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Loincet Submission

L. Submitted (21-APR-2001) Whitehead Institute/MIT Center for Genome Steearch, 320 Charles Street, Cambridge, MA 02141, USA on Jun 11, 2001 this sequence version replaced gi:13702847.

All repeats were identified using RepeatWasker:

All repeats were identified using RepeatWasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 205000; agarose-fp
Insert size: 206759; sum-of-contigs
Quality coverage: 9.6 in Q20 bases; sum-of-contigs
Quality coverage: 9.5 in Q20 bases; sum-of-contigs
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1531 4004: contig of 2474 bp in length
4005 4104; gap of 100 bp
4105 4104; octig of 127971 bp in length
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157807: contig of 16086 bp in length
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157908 173725: contig of 15818 bp in length
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173826 184364: contig of 10539 bp in length
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184465 206183: contig of 21719 bp in length
206184 206283: gap of 100 bp
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132176 135638: contig of 3463 bp in length
135639 135738: gap of 100 bp
135739 141621: contig of 5883 bp in length
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Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abcal)
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Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse abcal comparative sequencing and transgenesis studies revealing novel regulatory sequences
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (14-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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Matches 27; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
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/COGOLO_STATE_1
//COGOLO_STATE_1
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NLPARRNRARFGGGGSCHARATSRKGFFAQIVLDRAVFYCHGRONDPSLINGSTITUSPFGKREE
PWMINGOTFVRAMINGSPRANTERPROFERMENDELARATSREED
PWMINGOTFVRAMINGSSINGTRVAMINGSSILSTARMINIT
SPVPOSIVDENGNYTHROPSCHARATITITISFELLY
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VVFLIQERVSKAKHLOFISGYKPVIYMLSNFVWDMCNYVVPATLVIIIFICFQQKSYV
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                                                                                                                                                                                                                                                                                                           /product="ATP-binding cassette 1, sub-family A, member 1"81184. .210783
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LQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALPPSHEVNDA
IKQMKKLLKLTKSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVINNAIL
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RRFLWNCALSIVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGD
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QSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQD
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205427. 205558,206739. 206842,207361.
208135. 208378,209638. 210783)
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Homo sapiens BAC clone GS1-234B20 from 7q31.1-q31.3, complete
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Submitted (09-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis
Patent: Wo 0164874-A 50 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12425)
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7.6%; Score 27; DB 10; Length 278572; 100.0%; Pred. No. 0.00044; Live 0; Mismatches 0; Indels 0;
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The sequence of Homo sapiens BAC clone GSI-234B20
                                                                                                                                                                                              DNA
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                                                                                                                                                                                     Sequence 50 from Patent W00164874.
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/db_xref="taxon:9606"
a 3702 c 3566 g 2594
                                                                                        DD 103522 TTTATCTTTCAGTTAATGACCAGCCAC 103548
                                                                    88 tttatctttcagttaatgaccagccac 114
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AC006326.2 GI:4508133
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Waterston, R.H.
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restrict the sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Erric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@hhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selection: chloramphenicol NEIGHBORIG SEGENTA SEQUENCE INFORMATION:
NEIGHBORIG SEQUENCE INFORMATION:
The clone sequenced to the left is RP5-866N18, 200 bp overlap; clone sequenced to the right is CTA-343P13, 200 bp overlap. The actual start is unknown, the first known base of overlap is at base position 139224 of RG114A06; actual end is at 53881 of CTA-343P13.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 18427)
                                                                                                                                                                                                           JUNIATICE (UI-MAY-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (C. bases 1 to 18427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63108, USA
       Submitted (24-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is from the first BAC library from Genome Systems, Inc. (http://www.genomesystems.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-DEC-1999) Department of Genetics, Washington University, 444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Mar 24, 1999 this sequence version replaced 91:4138782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: H_GS234B20
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/db_xref="taxon:9606"
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/clone="GS1-234B20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- Genome Center
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Haplotypes: two
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                                                                                                                            5 (bases 1 to 18427)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPPING INFORMATION:
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FEATURES

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12068. .12557
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16020. 16285
/note="similar to EST T99055 (NID:9748792) ye67a02.sl"
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/note="match to EST N78828 (NID:91241529) zb17a04.s1"
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6379. .6740
/rpt_family="MalR"
7026. .7046
/rpt_family="AT_rich"
7246. .7544
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/rpt_family="AT_rich"
8042. .8132
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        'rpt_family="AT_rich"
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3523, 3646
                          436. .707 _
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298. .5473
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381. .4674
                                                                         /rpt_family="L1"
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524. .9818
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10955. .11122
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ALE SUBMITTED COMMISSION.

CBIO 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestEs clonerequestEstanger.ac.uk

CBIO 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requestEs clonerequestEstanger.ac.uk

On May 7, 2001 this sequence version replaced gi:13897175.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations.

Where differences are found these are annotated as variations.

Variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with an alternate as manil overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; SW:;

SWISSPROT; Tr:, TREMBL; WP:, WORNEPP; Information on the WORNEPP http://www.com.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="SLGTAGRVCNLTSRGMDSCEVMCCGRGYDTSHVTRMTKCGCKFH
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                                                                                                                                                                                                                                                         complement(16664...)=16891)
/gene="WUGSC:H_GS234B20.1"
complement(16664...)=16891)
/gene="WUGSC:H_GS234B20.1"
/note="WNT2; match to P09544 (PID:9139750); H_GS234B20.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear PRI 06-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                              note = "match to EST AA676311 (NID:92656833) zil0g04.sl"
                                                                                                 16072. .16571
/note="match to EST W88685 (NID:91404396) zh71e04.rl"
                                                                                                                                                                                                        16517. .16896
/note="match to EST W78848 (NID:91389395) zh51903.rl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA sequence from clone RP5-1098C18 on chromosome 1p36.23-36.33, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 24; DB 9; Length 184
100.0%; Pred. No. 0.022;
tive 0; Mismatches 0; Indels
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1 3991 c 3520 g 5795 t
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/protein_id="AAD28351.1"
/db_xref="GI:4731069"
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Best Local Similarity 100.C
Matches 24; Conservative
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Direct Submission
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     misc_feature
                                                      misc_feature
                                                                                                         misc_feature
                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL583882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
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http://www.sanger.ac.uk/HGP/Chrl
RP5-1098C18 is from the library RPCI-5 constructed by the group of better de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                     This sequence is the entire insert of clone RP5-1098C18 The true right end of clone RP11-154H17 is at 1402 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3462. 3740

/note="LiPB2 repeat: matches 5861. .6155 of consensus"

3890. 3991

/note="MER20 repeat: matches 118. .218 of consensus"

4018. .4076

4909. .4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314. .6690 note="LIMC3 repeat: matches 5437. .5825 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8740. .8801
/note="Alu repeat: matches 242. .298 of consensus"
8864. .9575
/note="LIMC3 repeat: matches 7021. .7738 of consensus"
9646. .10004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7301. 7532

/rocte="AluJo repeat: matches 63. 291 of consensus"

7540. 8738

/rocte="LIMC3 repeat: matches 5843. 7037 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="11M4 repeat: matches 3850. .3937 of consensus"
11945. .12188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4909. .4961

/note="L2 repeat: matches 2693. .2745 of consensus"

5551. .5610

5552. .5607

/note="14 copies 4 mor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT1A1 repeat: matches 1. .363 of consensus" 10015. .10187
/note="AluSp repeat: matches 132. .304 of consensus" /note="AluSp repeat: matches 1. .121 of consensus" /note="MuSp repeat: matches 1. .121 of consensus" 11856. _11944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6702. .6989
hotte="AluJb repeat: matches 13. .298 of consensus"
6922. .7237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2755. .2968
/note="MLT1B repeat: matches 1. .223 of consensus"
comptement(2762. .3096)
/note="match: STS: Em:HSPE03C10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5992. .7297
/note="AluSg repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="13 copies 10 mer gtgtgtgtgt 66% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .183. .1286
.note="MIR repeat: matches 41. .150 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MER8 repeat: matches 2. .238 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copies 4 mer gtgt 72% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                         /note="16 copies 2 mer tg 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /.uuce="49 copies 2 mer gt 72% conserved"
984. 1079
//note="24 copies /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copies 2 mer ca 75% conserved"
Further information can be found at
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p36.23-36.33"
/clone="RRS-1098C18"
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/note="29
                                                                                                                                                                                                          .90582
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'note="L1PA11 repeat: matches 5310. .6159 of consensus"
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16201. 16511
/note="Ally repeat: matches 1. 311 of consensus"
1722. 17364
/note="MER5A repeat: matches 20. 161 of consensus"
1875. 19068
/note="MER5A repeat: matches 8. 330 of consensus"
1875. 19966
/note="MITJC repeat: matches 1. 466 of consensus"
19575. 10996
/note="23 copies 4 mer gatg 64% conserved"
220098. 20108
/note="23 copies 28 mer 66% conserved"
22893. 23096
/note="LiMA9 repeat: matches 6028. .6211 of consensus"
13050. .13154
/note="LiMA9 repeat: matches 6199. .6303 of consensus"
13160. .13424
/note="LiMA repeat: matches 4374. .4642 of consensus"
13425. .13600
/note="Alusg/x repeat: matches 130. .305 of consensus"
13601. .13659
/note="LiMA repeat: matches 4648. .4709 of consensus"
13601. .13659
                                                                                                                                                                                                                                                                                                                                   14026. .14125

/note="10 copies 10 mer gagagaaaga 72% conserved"

14149. .14697

/note="LIMA repeat: matches 4694. .5255 of consensus"

/note="LIMB3 repeat: matches 6153. .6183 of consensus"

14956. .15266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LIMB3 repeat: matches 5792, .6153 of consensus"
15853, .16166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER91A repeat: matches 18. .196 of consensus"
30627. .30905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSg repeat: matches 18. .296 of consensus" 32695. .32726 /note="L2 repeat: matches 2466. .2497 of consensus" 33150. .33215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MER74A repeat: matches 1. .558 of consensus"
29282. .29456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MLT1D repeat: matches 17. .505 of consensus"
28426. .28538
                                                                                                                                                                                                                       /note="AluSq repeat: matches 1. .312 of consensus" 13976. 14147 //note="43 copies 4 mer ggaa 70% conserved" 13984. 14151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSp repeat: matches 1. .311 of consensus"
15267. .15610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 52. .114 of consensus" 34512. .34640
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8764. .29250
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Mote="MHR repeat: matches 81. .212 of consensus"
77909. .28364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22964. .23123

/note="16 copies 10 mer gaaagggaag 60% conserved"

23620. .23685

/note="MIR repeat: matches 20. .85 of consensus"

24243. .24699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="51 copies 4 mer ggaa 66% conserved"
                                                                                                                                                                                                                                                                                                                'note="6 copies 28 mer 72% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="CpG island"
/evidence=not_experimental
24326. .24541
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AF179296 123339 bp DNA linear HTG 08-OCT-1999
Homo sapiens, *** SEQUENCING IN PROGRESS ***, in ordered pleces.
AF179296
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Submitted (20-AUG-1999) Genome Analysis, Institute of Molecular
Submitted (20-AUG-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
contig 1: pos. 1 - 92151 contig 2: pos. 92152 - 123339 Inbetween a
gap of unknown size.
* NOTE: This is a 'working draft' sequence.
* This sequence as soon as it is available and
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                 1 (bases I to 123339)
Schudy,A., Platzer,M., Solilhabel,M., Koczan,D., Thiesen,H.-J.,
Merck-Rousseau,M.F., Baumgart,C., Menzel,U., Weber,J.,
Schattevoy, R. and Rosenthal.A.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
/note="FLAM_C repeat: matches 2. .127 of consensus" 34647. .34702 /note="2 copies 28 mer 96% conserved" 34648. .34703
                                                                                                                      7./note="FAM repeat: matches 116. .173 of consensus"
34766. .34906
                                                                                                                                                                                                                                                                                                                          /note="MLT2B repeat: matches 1. .73 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                           Query Match 6.7%; Score 24; DB 9; Length 90582; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                               //orde="14 copies 4 mer atat 96% conserved" 34703. .34760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
complement(2..144)
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complement(556..676)
/rpt_family="MIR"
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/rpt_family="MIR"
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1055. .1182
/rpt_family="alu"
1055. .1180
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.045. .1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                               326 ggaggagggaggaggaaggaag 349
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51335	rpt_type=inve 0551331 rpt_familue"x	ement(10	pt_ramily="SV 751232	.1232 .1232	15'-1333 229. 1333 rpt family="	15. 1335 232. 1335 rnt family="	2721346	1346	omplement(1332	lement(1339.	omplement	28 28 10ver	ement(1366. family="eya"	ement(14	11y=" nt(14 ]::-"	lement(143	Lement	505 "S	lement(1535	ramily="alu Lement(1566.	ramıly⇒"sv .1730	pt_tamily=" mplement(16 ot_famil:	6291797	pt_tamily= 961841	note="XNUN_REPEA 7991841	# @ #	evidence=n 9662073	note="SST_RE 7562847	rpt_f 756.	rpt_family="sva" 7583051	rpt_family=" 7582869	rpt_family="al 7772872	pt_ramily="sv mplement(2777		/evidence=not_experimental 28633047	
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rpt_family=" 8673048	rpt_tamily="al 8832954	pt_ramily="sv 942987	rpt_ramily=" 9132976	rpt_ramily="sva 9623017	5 V C	73208	Ly= t(3	rpt_ramlly="LIMC3 1373205 rpt familv="11mc4	.3205 .3205 .milu-"11mg2	ement(3142	ement(3371		camily="Mik ement(3405. familv="mir	3721	7623900	.4055 4055	1084318	rpt_ramily="MSTB 1084246	/rpt_ramily="MSTA" complement(41104245)	TPC_tamily= msca Omplement(4154. rnt family="tholl	114246 ote-"XPOUND"	evidence=not_ex 2904414	rpt_family="alu" 3194619	rpt_ramily="Alu 3224449	rpt_tamily="s 3224491	rpt_ramily="a 3324484	<pre>tPt_lamily="ALU omplement(4342.</pre>	19C_tamil1y= SV 3454706 rnt_trmo_innor	3474706	12	1Pt_type=1Nver 3514417 rnt typo=innor	465460	5244579 rpt family="	095070 pt type=inv	5066
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bousladter, B., Brown, A., Burkett, G., Bousladter, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Colymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grand, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Larcoque, K., Langors, B., Heaford, A., Horton, L., Klein, J., Larcoque, K., Langaran, R., Mores, C., Kann, L., Karatas, A., Klein, J., Larcoque, K., Langaran, R., Mores, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Langaran, R., Morenan, R., Morecarhy, M., McEwan, P., McGurk, A., McKernan, K., Morheeters, R., Mardyn, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T., Mihova, T., Mihova, T., Mihova, T., Mihova, T., Miranda, C., Flerre, N., Flerre, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, Woll, W., Vo, M., Wilson, B., Wu, X., Wyman, D., Ye, Woll, M., Vola, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, Woll, M., More, M., Woll, R., Woll, M., Will, M., W., Wyman, D., Ye, Woll, M., Woll, R., Woll, M., Will, M., Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 8, clone RP11-293L6, complete sequence. AC036144
AC036144.7 GI:18104887
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4709. .5068
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Direct Submission

AL Submitted (10-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Escarch, 320 Charles Street, Cambridge, MA 02141, USA

Escarch, 320 Charles Street, Cambridge, MA 02141, USA

Escarch, 10-127270

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., DeArellano, W., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Graham, L., Grand, Pleare, N., Ginde, S., Gord, S., Gord, S., Goyette, M., Graham, L., Grand, Pleare, N., Hagos, B., Heaford, A., Horton, L., Hulme, M., Lilev, I., Johnson, R., Jones, C., Kamat, A., Karlas, A., Kells, C., LaRocque, K., Jones, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McGernan, K., McPheeters, R., Rieb, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Severy, P., Spencer, B., Santos, R., Schauer, S., Schupback, Roman, J., Roy, A., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
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Submitted (08-OCT-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Essearch, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Campopiano, A., Characro, B., Characro, B., Chope, I., Campopiano, A., Characro, B., Chore, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamart, A., Karatas, A., Kells, C., LaRocque, K., Landazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Merquis, N., Matthews, C., Macdonald, P., Major, J., Merquis, N., Matthews, C., Mercaron, C., Mercaron, C., Mercaron, C., Mercaron, Y., Mengay, V., Murphy, T., Naylor, J., Norla, V., Mengan, C. H., O'Connor, T., O'Donnell, P., O'Nail, D., Norla, C., Retta, R., Reback, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stenas, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Zainoun, J., Lander, J., Lande
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norban, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosettl, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stange-Thomann, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Thocdore, J., Topham, K., Travers, M., Travis, N.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jan 10, 2002 this sequence version replaced 91:15983570.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washing.con.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu

repeat\_region

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T7 end overlaps AC009941 [WICGR Project L1987] by 103216 bp. Location/Qualifiers
Contact: sequence_submissions@genome.wi.mit.edu
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14034. .14057
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6610. 6647
7rpt_family="(TTG)n"
complement(6648 . 8549)
/rpt_family="LiPA7"
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/rpt_family="AT_rich"
complement(10474. .10599)
/rpt_family="MIR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(12759. .13088)
/rpt_family="MER7A"
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/rpt_family="L1"
10180, .10236
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'omplement'/177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(8549. .9721)
/rpt_family="L1"
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                                                clone name: 293_L_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="AT_rich"
complement(12357. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="AT_rich"
                                                                                                                                                                                                      /clone="RP11-293L6"
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                              Center project name:
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Direct Submission

Loud (09-0CT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 13A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequesf@sanger.ac.uk mnquery@sanger.ac.uk Clone requests: clonerequesf@sanger.ac.uk

On Aug 21, 2000 this sequence version replaced gi:9856693.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature. Low.
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA sequence from clone RP11-5N23 on chromosome 10p14-15.3 Contains ESTs, GSSs, STSs and a CpG island. Contains the 5' part of the PRKCQ gene for protein kinase C theta and a novel gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following abbreviations are used to associate primary accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP11-5N23 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP11-5N23 is at 132741 in this sequence. The true left end of clone RP11-55478 is at 102011 in this sequence. The true right end of clone RP11-55478 is at 100 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.urk/ROP/Chr10
RP11-5N23 is from the library RPCI-11.1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORWPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
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                                                                                                                         6.7%; Score 24; DB 9; Length 127270; 100.0%; Pred. No. 0.024; Live 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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complement(14859. .14987)
/rpt_family="L2"
15347. .15525
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                       Db 18870 GGAGGAGGAGGAAGGAAG 18847
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/map="p14-15.3"
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                                                                                                                                                                                        24; Conservative
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/ Match 6.7%; Score 24; DB 9; Length 132741; Local Similarity 100.0%; Pred. No. 0.024; nes 24; Conservative 0; Mismatches 0; Indels 0;
misc_feature
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Matches 24;
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TEIWLELKPOGRULMARYFLENGRYWQIIVGGKNUDLISETATYELYSLAERCRKNNGK
EFTATFFPQFTFCSVCHEFVWGLNKQGYQCRQCRQCRAALHKKCIDKYIAKCTGGALVHVKCH
BFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCRQCRAALHKKCIDKYIAKCTGGALNSRE
YMEHKBREKTIDMHRRYXYNXKSPTFCEHCGTLLWGLARQGLKCDACGMNVHHRCQTK
VANLCGINQKLWAEALAMIESTQQ"
complement (757.868)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSPFLRIGLSNFDCGSCQSCQGEAVNPYCAVLVKEYVESENGQM
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="continued in bA563J2 (AL137145), gene bA563J2.2
match: proteins: Sw:004759 Sw:002111 Tr:092333 Sw:P09215
Sw:Q05655 Sw:P28867 Tr:Q15144 Sw:P34722 Wp:B0545B
Tr:061225 Tr:062569"
                                                                                                                                                                                                                                                                                                                        complement(join(<510. .619,6158. .6287,11510. .11595,
11695. .11726,12871. .13033,21911. .21971,25470. .25669,
29493. .29610))
                  complement(join(<510. .619,6158. .6287,11510. .11595,
11695. .11726,12871. .13033,21911. .21971,25470. .25669,
29493. .29610,94686. .94767))
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Em:L07032 Em:L07860 Em:L07861 Em:x60304 Em:AB011812
Em:AF219629 Em:M18330 Em:RF251036 Em:M69042 Em:D10495
match: ESTs: Em:AIS28522 Em:AAIS3683 Em:AI326731"
/product="hA5N23.1" (protein kinase C theta)"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 2315. .2745 of consensus" 0243. .10408
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/note="L2 repeat: matches 2651. .2691 of consensus"

2863. .3158

/note="Alusx repeat: matches 1. .298 of consensus"

3268. .3555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER66A repeat: matches 1. .478 of consensus"
1911. .1943
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1141. .11319
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Arote-"AluJo repeat: matches 3. .311 of consensus"
6886. -7558
/note-"MIR_repeat: matches 28. .205 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="MER33 repeat: matches 4. ,324 of consensus"
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//note="L2 repeat: matches 566. .2144 of consensus"
8826. .10196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1191. .2500
/note="AluSx repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .287 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 81. .115 of consensus"
2191. .2500
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note="MIR repeat: matches 20. .123 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14842. .14961
/note="20 copies 6 mer atatat 67% conserved"
14873. .14968
/note="8 copies 12 mer 67% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/product="bash23.1" (protein kinase C theta)"
/protein id="CaC12904.1"
/db_xref="G1:10799537"
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                                                                                                                                                                                                                                                                                                        /gene="PRKCO"
                                                                                                      /gene="PRKCO'
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/note="AluJb repeat: matches 3. .273 of consensus"
20685. .20902
7.note="LiMC5 repeat: matches 7726. .7931 of consensus"
20910. .20960. .20132
7.note="US repeat: matches 6. .55 of consensus"
7.note="LiM2 repeat: matches 7566. .7727 of consensus"
21640. .22146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIME1 repeat: matches 5904. .6168 of consensus" .33320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER49 repeat: matches 449. .738 of consensus" complement(34143. .34519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28312. .28514
/note="L2 repeat: matches 2437. .2665 of consensus"
32062. .32097
/note=="18 copies 2 mer tt 97% conserved"
32445. .32674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Allsx repeat: matches 3. 310 of consensus" 33460. 33555
/note="48 copies 2 mer at 66% conserved" 33474. 33545
/note="6 copies 12 mer 77% conserved" 33475. 33558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0016="MIR repeat: matches 31. .191 of consensus"
23514. 23599
23514. 23599
23553. .24183
7.001e="AluSq repeat: matches 1. .231 of consensus"
24487. 24558
7.001e="AluSq repeat: matches 25934"
7.001e="Copies 36 mer 94% conserved"
25934. .26379
                                                                                                                                                                /note="12 repeat: matches 2579, .2701 of consensus"
18266, .18551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="LOR1b repeat: matches 1. .461 of consensus"
                                                                                                                                                                                                        /note="AluJo repeat: matches 1. 286 of consensus"
19367. 19666
/note="AluY repeat: matches 1. 301 of consensus"
19870. 20145
/note="Alo copies 6 mer tttctt 57% conserved"
19871. 20122
                                                                                                                         /note="AluSp repeat: matches 1. .308 of consensus"
16510. .16637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="14 copies 6 mer tatgta 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19897. .20141
/note="5 copies 49 mer 66% conserved"
19985. .20059
/note="15 copies 5 mer ttctt 68% conserved"
20148. .20418
                                                                                                                                                                                                                                                                                                                                       /note="7 copies 36 mer 67% conserved" 19872. 20147 /note="23 copies 12 mer 60% conserved" 19800. 20141 /note="3 copies 84 mer 74% conserved" /note="3 copies 84 mer 74% conserved"
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22859. .23008
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27276. .27777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AQ541207"
complement(22776. .23021)
15109. .15456
/note="match: GSS: Em:AQ131538"
15123. .15920
                                                                                     'note="match: GSS: Em:AQ897533"
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                                                                                                            16324
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ALEACY SUBMISSION

ALEACY CARD 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

ON NOV 20, 2001 this sequence version replaced gi:15808147.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with a mall overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following assembly was recused to associate primary accession numbers given in the feature table with their source databases: Em: EMBL: Sw:, Area, Canner or the WORMPEP! Information or the WORMPEP http://www.earner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.uk.canner.ac.u
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/note="Single clone region. Assembly confirmed by restriction digest data." complement(134064. 134068)
/note="Single clone region. Assembly confirmed by restriction digest data." complement(134070. 134075)
/note="Single clone region. Assembly confirmed by restriction digest data." complement(134077. 134087)
/note="Single clone region. Assembly confirmed by restriction digest data." complement(134077. 134087)
/note="Single clone region. Assembly confirmed by restriction digest data."
                                                                                                                                                                                                                                                                        AL163512 134334 bp DNA linear ROD 17-NOV-2001
MOUSE DNA sequence from clone RP21-466E12 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP21-468E12 is from the RPCI-21 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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be approximately 280bp by restriction digest data."
114512
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/chromosome="X"
/clone="RP21-468E12"

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15023
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AL353893 137072 bp DNA linear HTG 10-JUL-2001
Homo sapiens chromosome 1 clone RP5-1108E5, *** SEQUENCING IN
PROCRESS ***, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 137072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 15, 2000 this sequence version replaced gi:8052073.
                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 134274 bases at least Q40
Consensus quality: 135563 bases at least Q30
Consensus quality: 135563 bases at least Q20
Insert size: 136572; sum-of-contigs
Insert size: 136372; sum-of-contigs
Quality coverage: 4.52x in Q20 bases; sum-of-contigs Quality
coverage: 4.50x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                         6.7%; Score 24; DB 10; Length 134334;
100.0%; Pred. No. 0.024;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68025 68024; gap of 100 bp 68025 71010; contig of 2986 bp in length 71011 71110; gap of 100 bp 100 bp 71111 89837; contig of 18727 bp in length 89838 89937; gap of 100 bp 89938 113010; contig of 23073 bp in length 113011 11310; gap of 100 bp 113011 113072; contig of 23962 bp in length.
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4386 67924: contig of 63539 bp in length
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41709 a 26034 c 25611 g 40980 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: SC
Web site: http://www.sanger.ac.uk
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Matches 24; Conservative
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1174.752 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                      1736436 seqs, 858457221 residues
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    nucleic search, using sw model

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21. /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NRA1981.DAT:\*
32. /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NRA1981.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human ABC1 gene ex	Human ABC1 genomic	Nucleotide sequenc	Partial human ABC1					
	ID	AAC69132	AAF92831	AAF24680	AAF24702	AAF24685	AAF24686	AAF24707	AAF24708	AAS04035
	ВС	21	22	22	22	22	22	22	22	22
	Query re Match Length DB I	44.5 10545	183999	10442	10442	10474	10474	10474	10474	446
œ	Query Match	44.5	44.5	21.6	21.6	21.6	21.6	21.6	21.6	16.8
	Score	159	159	77	77	77	77	77	77	9
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## ALIGNMENTS

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Human ABC1 cholesterol transporter; chromosome 9q31; promoter; ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangler disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alsmann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; ss.
                                                                                                      Human ABC1 gene exon 1 (promoter).
                      AAC69132 standard; DNA; 10545 BP.
                                                                                                                                                                                                                                                                                                                                                                               99US-0138048.
                                                                                                                                                                                                                                                                                                                                        15-MAR-2000; 2000WO-IB00532.
                                                                                                                                                                                                                                                                                                                                                                    99US-0124702.
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                                                                              29-JAN-2001 (first entry)
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08-JUN-1999;
17-JUN-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                21-SEP-2000.
                                                   AAC69132;
RESULT
AAC69132
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(first entry)

17-MAY-2001

Human ABC1 genomic DNA.

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The invention relates to the human ABCI cholesterol transporter protein CC (BB8082) and to nucleic acid sequences (C69120) which encode it. ABCI is a member of the APP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly citracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol lefflux from the cell. The gene encoding ABCI is involved in cholesterol efflux from the cell. The gene encoding ABCI is involved in cholesterol efflux from the cell. The gene are associated converted tisease (TD) and familial HDL deficiency (FHA). These diseases of and familial HDL deficiency (FHA). These diseases of and familial HDL deficiency (FHA). These diseases of a autosomal dominant trait. LOW levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease. Darkicularly corromary artery disease, but also cerebrovascular disease. Coronary restenosis, and peripheral vascular disease. Coronary restenosis, and peripheral vascular disease. Cardiovascular disease. The invention provides genetic constructs and transgenic cells and mon-human animals comprising human ABCI nucleic cardiovascular disease comprising the administration of an expression concompasses compounds which minic ABCI expression and methods of sorteening for such compounds. Conformation and cancer correspond and disease compounds which minic ABCI expression and methods of sorteening for such compounds corrected cardiovascular disease, coronary restenosis or peripheral vascular disease, coronary restenosis or peripheral vascular disease, coronary restenosis or peripheral disease. Coronary artery disease associated carebrovascular disease, coronary restenosis or peripheral disease, coronary restenosis or peripheral vascular disease, coronary restenosis or peripheral vascular disease, coronary restenosis or peripheral vascular disease, Huntington's disease
                                                                                                                                                                              New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                                                           Hayden MR, Wilson AR, Pimstone SN;
                                                                                                                                                                                                                                                                                  Claim 50; Fig 12; 229pp; English.
(UYBR-) UNIV BRITISH COLUMBIA. (XENO-) XENON BIORESEARCH INC.
                                                                                                                                                                                                                                    disease and cancer -
                                                                                                                           WPI; 2000-587528/55
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ő 8240 tgittggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 8299 199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258 Gaps . 0 44.5%; Score 159; DB 21; Length 10545; 100.0%; Pred. No. 2.3e-68; Live 0; Mismatches 0; Indels 0; 8360 ggggattggaggagggagggagggaaggaagctgtgttg 8398 319 ggggattggaggaggaggaggaaggaagctgtgttg 357 Conservative Best\_Local Similarity Matches 159; Conserv Query Match g ò ò g ò

Sequence 10545 BP; 2647 A; 2225 C; 2411 G; 3256 T; 6 other;

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AAF92831
ID AAF92831 standard; DNA; 183999 BP.
                                              AAF92831;
7
RESULT
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diagnosed as having a lower than normal high density of processions in properced. In properced. In the Land of the configuration of a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease. Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity . High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCl; ds. 53328 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 53387 199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258 0; Gaps Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other; The present invention relates to a method for treating a patient 44.5%; Score 159; DB 22; Length 183999; 100.0%; Pred. No. 2.3e-68; tive 0; Mismatches 0; Indels 0; Clee SM; 53448 ggggattggaggaggagggagggaaggaagctgtgttg 53486 319 ggggattggaggagggagggagggaaggaagctgtgttg 357 Nucleotide sequence of a human ABC1 polypeptide. Hayden MR, Brooks-Wilson AR, Pimstone SN, AAF24680 standard; DNA; 10442 BP. Claim 8; Fig 1; 317pp; English. (UYBR-) UNIV BRITISH COLUMBIA 15-MAR-2000; 2000US-0526193. 23-JUN-2000; 2000US-0213958. 01-SEP-2000; 2000WO-IB01492. 99US-0151977 (XENO-) XENON GENETICS INC (first entry) Matches 159; Conservative WPI; 2001-244356/25. Query Match Best Local Similarity WO200115676-A2. Homo sapiens, 01-SEP-1999; 08-MAR-2001 20-APR-2001 AAF24680; AAF24680 рp g ò δ ŏ ΩX

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AAF24702

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The present sequence encodes a human adenosine triphosphate (ATP)
binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
commembranes and utilises ATP hydrolysis to transport a wide variety of
substrates across the plasma membrane. ABC1 is a pivotal protein in
the apolipoprotein-mediated mobilisation of intracellular cholesterol
stores, ABC1 is defective in Tangier disease, a genetic disorder
characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
localised to chromosome 9422-9431. The ABC1 genes and proteins are
useful for developing pharmaceutical agents for the treatment of heart
disease and other disorders associated with hypercholesterolemia and
atherosclerosis. The genes are useful for developing screening assays to
screen for compounds that regulate the expression of genes associated
with cholesterol transport. The genes and proteins are also useful for
are also useful as diagnostic indicators of cardiovascular disease and
cher disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
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Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia;
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                                                                                                      atherosclerosis; cholesterol transport; ss.
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                                                                                                                                                                                                                                 Location/Qualifiers
291..7076
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atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of
                                                                                                                           Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangler disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 21.6%; Score 77; DB 22; Length 10442; Local Similarity 99.2%; Pred. No. 4.8e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other disorders associated with hypercholesterolemia.
                                                                                                  Nucleotide sequence of a human ABC1 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garvin M;
                                                                                                                                                                                                                                                       Location/Qualifiers
AAF24702 standard; DNA; 10442 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0140264.
99US-0153872.
99US-0166573.
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14-SEP-1999;
19-NOV-1999;
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                                                                    20-APR-2001
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Gaps

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Length 10474;

Score 77; DB 22; Length 10 Pred. No. 4.8e-28; 0; Mismatches 1; Indels

21.6%; 99.2%;

Query Match
Best Local Similarity 99.2'
Matches 127; Conservative

131 agctctggccgctgccttccagggctcccgagccacacgctggcgtgctgaggga 190

261 agetetggeegetgeetteeagggeteeegageeacacacgetgggegtgetggetgaggga 320

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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the mobilisation of intracellular cholesterol stores. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome pharmaceutical agents for the treatment of heart disease and other metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                                                                                         Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "defective ABC1 polypeptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
323..7108
                                                                                                                                                                               AAF24685 standard; DNA; 10474 BP.
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                                                                    gacaaaca 258
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19-NOV-1999;
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangter disease patient. ABC1 resides in cell membranes and utilises ATP pared disease patient, a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                          Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
                                                                                                                                                                                                                                           Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           /product= "defective ABC1 polypeptide"
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                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 323..7108
                                                                                                              AAF24686 standard; DNA; 10474 BP.
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99US-0153872.
99US-0166573.
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251 gacaaaca 258
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14-SEP-1999;
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Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

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disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
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                                                                                                                                                                                                  191 acatggcatgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaa 250
                                                                                                                                                                                                                                                                      261 agetetggeegetgeetteeagggeteeegageeacaegetgggegtgetggetgaggga 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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                                                                                                                                         21.6%; Score 77; DB 22; Length 10474; 99.2%; Pred, No. 4.8e-28;
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                                                                                                                                                                       1; Indels
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                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                        127; Conservative
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                                                                                                                                               Query Match
                                                                                                                                                              Local
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                  present experient (ABC) I polypeptide, and is isolated from a rangler disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotral protein in the apolipoprotein mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in rangiler disease, a genetic disorder characterised by abnormal application of intracellular cholesterol stores. ABC1 is defective in rangiler disease, a genetic disorder characterised by abnormal phot-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol as diagnostic. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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       present sequence encodes a human adenosine triphosphate (ATP)
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/product= "defective ABC1 polypeptide"
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19-NOV-1999;
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The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from
a Tangier disease patient. ABC1 resides in cell membranes and utilises
a Tangier disease patient. ABC1 resides in cell membranes and utilises
plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABC1 is defective in
Tangier disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
plasmacceutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atheroscierosis. The
genes are useful for developing screening assays to screen for compounds
that regulate the expression of genes associated with cholesterol
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                                                                                              polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
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/product= "Human ABC1 protein, amino acids 1 to 60"
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cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                              Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.6%; Score 77; DB 22; Length 10474; 99.2%; Pred. No. 4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
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                                                                                                                                                             Claim 30; Page 165-172; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               associated with hypercholesterolemia.
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 Oram JF,
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                           WPI; 2001-137811/14.
 Lawn RM, Wade D,
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                                                P-PSDB; AAB31367
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Human; cytokine; cell proliferation; cell differentiation; growth factor;
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                                                                                                                                                                                                                                                                                                                                                                             The sequence represents the partial coding sequence of human ABC1, which encodes amino acids 1-60 of the human ABC1 protein. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of coholesteroi. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                Brewer HB;
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Duverger N, Jaye M, Searfoss GH, Remaley A, B
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                                                                                                                                                                                                                                                                                     New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                            Example 2; Page 167; 368pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA09200 standard; cDNA; 7086 BP.
                  26-OCT-2000; 2000WO-EP10886.
                                                    26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
                                                                                                                 (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2002 (first entry)
                                                                                                                                                                                                                             WPI; 2001-316327/33.
                                                                                                                                                                                                                                                   P-PSDB; AAU02176
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                                                                                                                                                      Denefle P,
                                                                                                                                                                          Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                            Dean M;
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qq
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Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.

Human polynucleotide SEQ ID NO 2196.

(first entry)

06-NOV-2001

AAK52667;

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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. Concleotide of the invention and methods of detecting the nucleotides or polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; sem cell growth factor activity; hemoretopiesis regulatory activity; tissue growth activity; commondulatory activity; activin- or inhibin-related activities; commondulatory activity; activin- or inhibin-related activities; commondulatory activity; activin- or inhibin-related activities; commondulatory activities, polypeptides or may be not conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, hematopoietic disorders (e.g., methodic or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthitis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial isochemia, bone disorders (e.g., osteoporosis), and abnormal creating infections in addition to immune disorders to muchaic acids encoding them) may be used to promote wound the manipulate stem cells in citture to give rise to neuropeintal and fungal infections in addition to immune disorders to manipulate stem cells in culture to give rise to neuropeintal and fungal infections in addition to immune of insured to a second to a sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                         Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that can be used to augment or replace cells damaged by illness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 833-835; 1963pp; English
                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT;
                                                     05-FEB-2001; 2001WO-US03800.
                                                                                                    20000S-0496914
                                                                                                                            27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                            WPI; 2001-457740/49.
                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                              P-PSDB; ABB11956
                                                                                                    03-FEB-2000;
09-AUG-2001.
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Ma Y;

Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;

19-JUL-2000; 2000US-0620325. 01.SEP-2000; 2000US-0654936. 15-SEP-2000; 2000US-0653561. 20-OCT-2000; 2000US-063325. 30-NOV-2000; 2000US-0728422.

(HYSE-) HYSEQ INC.

2000US-0560875 2000US-0598075

2000US-0496914

03-FEB-2000; 20-JUN-2000; 27-APR-2000;

05-FEB-2001; 2001WO-US04098

WO200157190-A2.

09-AUG-2001

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -

WPI; 2001-476283/51. P-PSDB; AAM79534.

Claim 1; Page 4558-4560; 6221pp; English.

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activinihibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                 inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 16.8%; Score 60; DB 22; Length 7086; Best Local Similarity 100.0%; Pred. No. 1.1e-19; Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD21326 standard; DNA; 7260 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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0; Gaps

199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258 

δλ

AAK52667 standard; cDNA; 7086 BP

11 RESULT 1
AAK52667
ID AAK52

Ouery Match 16.8%; Score 60; DB 22; Length 7086; Best Local Similarity 100.0%; Pred. No. 1.1e-19; Matches 60; Conservative 0; Mismatches 0; Indels

ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory disease; antlinflammatory; antilipaemic; antipsoriatic; dermatological; Tangler disease; coronary heart disease; diagnosis; gene therapy;

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Human; ATP binding cassette transporter 1; ABC1; coronary heart disease; dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing and treating lipid disorders, cardiovascular diseases diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lbeta (IL-lbeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis and septic shock. The present sequence is human ABC1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                      Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                                                                                                                                                                                                                                                             /product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 16.8%; Score 60; DB 1 Similarity 100.0%; Pred. No. 1.1 60; Conservative 0; Mismatches
                                                                                                                                                                                                                                                         Location/Qualifiers 321..7106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2000; 2000EP-0105820
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                                                     28-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmitz G, Bodzioch M;
                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-640388/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAE13022.
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                EP1136552-A1
                   AAD21326;
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The present sequence is that of cDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AME0227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAI70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 Nterminal amino acids to the encoded ABC1 protein (see AME0228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in different Tangier kindreds. In the variant genes (numbering as in different Tangier kindreds. In the variant genes (numbering as in different Tangier kindreds. In the variant genes (numbering as in different Tangier kindreds. In the variant genes (numbering as in different Tangier the amno acid sequence of ABC1 and therefore position 1345, A is changed to G at position 2589 or G is changed to C at position 1345, or any combination of these. All of these polymorphisms alter the amno acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G and G3456C) are significantly increased in vitro AppA-I mediated efflux of cholesterol from monounclear phagocytes, a catcom catcom and A2589G and G3456C) are significantly increased in a population of eather the and any addition the acid sequence of a population of acid sether the and any addition of the variants (G596A, and A2589G and G3456C) are significantly increased in a population of methalished province and account the acid and account the acid and account the acid and account the acid and account the acid and account the acid and account the acid and account the acid and account the acid and account the acid and account the acid account the acid account the acid account the account the account the account the account the account the account the account the acco
                                                                                                                                                                                                                                                                                                 /*tag= b
/note= "alternative open reading frame of AAI70314"
replace(976,A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 26-28; 41pp; English.
                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           replace(1516,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(2969,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(3836,C)
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                                                                                                             polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER AG.
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                                                                                                                                                           Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                             variation
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                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                         CDS
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Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Human ATP binding cassette transporter 1 (ABC1) cDNA.

07-JAN-2002 (first entry)

XX

AAI70315 standard; cDNA; 7260 BP

RESULT 13 AAI7031

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0; Gaps

Length 7260;

Score 60; DB 22; I Pred. No. 1.1e-19;

Best Local Similarity

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Query Match Matches 

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                                                       199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258
                                                                                    327 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 386
                            Gaps
                              ;
0
Length 7260;
                              0; Indels
               1.1e-19;
DB 22;
                100.0%; Pred. No. 1.1 tive 0; Mismatches
   Score 60;
    16.8%;
                            60; Conservative
                  Similarity
      Query Match
                     Best Local
                                 Matches
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Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss. Human polynucleotide SEQ ID NO 228. AAK51683 standard; cDNA; 7281 (first entry) 06-NOV-2001 AAK51683; AAK51683 g

2000US-0663561. 2000US-0693325. 2000US-0728422. 2000US-0496914. 2000US-0560875. 2000US-0598075. 2000US-0620325. 05-FEB-2001; 2001WO-US04098. 2000US-0654936. WO200157190-A2 Homo sapiens. 27-APR-2000; 20-JUN-2000; 15-SEP-2000; 20-OCT-2000; 03-FEB-2000; 19-JUL-2000; 01-SEP-2000; 09-AUG-2001 

Asundi V, Zhou P, Xu C, Cao Y, ang J, Ren F, Chen R, Wang ZW; Weihrman T, Goodrich R; Drmanac RT, ď Wang D, Yang Y, Liu C, rang YT, o'A' Xue AJ, Shao

(HYSE-) HYSEQ INC.

30-NOV-2000;

Ma Y;

WPI; 2001-476283/51. P-PSDB; AAM78550 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy

Claim 1; Page 1086-1096; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to sytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) Superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is concerd on chromosome 9931, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, think two genetic HDL (high density lipoprotein) deficiency disorders, and istinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular classase, coronary restenosis, and peripheral vascular disease.

Conversely, a high level of HDL Has protective effects against cardiovascular disease. The invention provides genetic constructs and

Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;

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                                                                                                                                                                                                               Human ABC1 cholesterol transporter; chromosome 9431;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; rangier disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary retenosis; cerebrovascular disease; peripheral vascular disease; Lalzeimer's disease; huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
                                                                                                                                                                                           Human ABC1 cholesterol transporter FHA-3 mutant cDNA (delta 5752-5757).
                                           New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                      Gaps
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Length 7281;
 16.8%; Score 60; DB 22; I 100.0%; Pred. No. 1.1e-19;
         100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayden MR, Wilson AR, Pimstone SN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examples; Page -; 229pp; English.
                                                                                                                            AAC69388 standard; cDNA; 7857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (XENO-) XENON BIORESEARCH INC
                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0138048.
99US-0139600.
99US-0151977.
                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2000; 2000WO-IB00532.
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                                                                                                                                                                         (first entry)
                         60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-587528/55.
   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               WO200055318-A2.
                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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17-JUN-1999;
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                                                                                                                                                                         29-JAN-2001
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                                                                                                        12
                         Matches
                                                                                                        RESULT 1
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ABC1 gene. Human ABC1 proteins disease, cue control proteins and the research transversallar disease, especially coronary artery disease, or prevent cardiovascular disease, especially coronary artery disease, disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheiner's disease, Niemann-Pick disease, Huntingfon's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid acid with the exact sequence as GenBank Accession No: CAA10005.1 and X75926, and the nucleic present sequence represents converted as many altered control of a mutant human ABC1 cholesterol transporter associated with an altered disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "the coding sequence continues beyond nucleotide 3341, possibly till position 6860 as identified by translating the present sequence; part of the corresponding protein is missing and nucleotide 3341 corresponds to the last amino acid residue (position 1089) as indicated in the specification.
transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                Note: The present sequence is not shown in the specification, k
derived from the native human ABC1 cDNA shown on pages 157-160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 21; Length 7857; Pred. No. 1.1e-19; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.8%; Score 60;
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100.0%; Pic
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Matches 6
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The invention relates to a new method for inhibiting cholesterol uptake in the gut that comprises administration of an inhibitor of an ABC1 protein. The method is useful for: lowering levels of LDL (low density lipoprotein) cholesterol by reducing the activity of ABC1 protein in the intestinal cells and the abundance of the ABC1 protein in the individual by inhibiting the activity of the protein; identifying drugs that can lower serum cholesterol and LDL levels comprises assaying the drug to test if it can bind to an ABC1 protein; testing LDL cholesterol lowering agents; and for modulation of ABC1 biological activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCl; ss.
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                                                                                                                                                                                               New method for inhibiting cholesterol uptake in the gut comprises
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   Cook M, Gray-Keller MP, Hayden MR, Pimstone S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a human ABC1 nucleotide sequence.
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                                                                                                                                                                                                                             administration of an inhibitor of an ABC1 protein
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No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.8%; Score 60; DB 100.0%; Pred. No. 1.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or RXR-mediated transcriptional activity -
                                                                                                                                                                                                                                                                                          Disclosure; Page 34-36; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 317pp; English.
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                                                                                              2001-335779/35.
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Attie AD, Cook N
Brooks-Wilson A;
                                                                                                                               P-PSDB; AAB62691
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The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is amember of the AFP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangter disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
cerebrovascular disease; peripheral vascular disease;
Allahamer's disease; Niemann-Pick disease; Huntington's disease;
X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ABC1 cholesterol transporter FHA-1 mutant cDNA (delta 2151-2153)
                                                                                                                                                                                                                                                                                                                   199 tgttggcctcagctgaggttgctgctgtggaagaacctcactttcagaagaagacaaaca 258
                                                                                                                                                                                                                                                                                                                                         New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                           16.8%; Score 60; DB 22; Length 7860; 100.0%; Pred. No. 1.1e-19; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                         Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC69387 standard; cDNA; 7861 BP
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99US-0139600.
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                                                                                                                                                                                                                                                                                    Conservative
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P-PSDB; AAB38106.
                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                      Matches
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involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, can distinguishable in that TD is an autosomal recessive disorder, while are distinguishable in that TD is an autosomal recessive disorder, while cholesterol") in the blood correlate with a high risk of cardiovascular disease, coronary restencists, and peripheral vascular disease. Coronary restencists, and peripheral vascular disease. Coronary restencists, and peripheral vascular disease. Coronary restencists, and peripheral vascular disease. Coronary restencists, and peripheral vascular disease. The invention provides genetic constructs and cardiovascular disease. The invention provides genetic constructs and cardiovascular disease comprising the administration of an expression corompasses compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic activity is compassed risk for cardiovascular disease due to polymorphisms in the increased risk for cardiovascular disease due to polymorphisms in the carebrovascular disease, coronary restenosis or peripheral vascular disease, cerbrovascular disease, coronary restenosis or peripheral vascular disease, coronary restenosis or peripheral vascular disease, sepecially coronary artery disease, with ABC1 biological activity, such as Alzheimer's disease, Nemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. Che invention specifically excludes proteins with the exact sequence as GenBank Accession No: CANJO005.1 and X75926, and the nucleic certain sequence represents conditions and interned benefits and peripheral and with an altered cholesterol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transporter associated with an altered cholesterol level and therefore an altered risk of cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ABC1 cholesterol transporter; chromosome 9931;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prognosis; prophylaxis; drug screening; transgenic animal; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 cDNA shown on pages 157-160.
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Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.8%; Score 60; DB 21; Length 7861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC69120 standard; cDNA; 7864 BP
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Best Local Similarity
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The invention relates to the human ABC1 cholesterol transporter protein CC (1898082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transports, particularly correctins, and plays a crucial role in cholesterol trafficking in monocytes and fibroblasts, being intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol trafficking in the cell in the space encoding ABC1 is corrected on chromosome 9q1, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, are distinguishable in that TD is an autosomal recessive disorder, while FH is inherited as an autosomal dominant trait. Low levels of HDL ("good carelate with a high risk of cardiovascular chlease, coronary restences!, and peripheral vascular disease. particularly coronary artery disease, but also cerebrovascular cardiovascular disease. particularly coronary artery disease, but also cerebrovascular cardiovascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. Compasses compounds which has protective effects against cardiovascular disease comprising the administration of an expression cardiovascular disease compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which mimic ABC1 activity and methods of screening for such compounds of increased risk for cardiovascular disease, especially ocronary artery disease. Coronary actery disease. They may also be used in the treatment of diseases. They may also be used in the treatment of disease. They may also be used in the treatment of disease. They may also be used in the exact amino activity sequences and GenBank Accession No: CAJONOS: 
                                                                                                                                                                                                                                                                                                               New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 157-160; 229pp; English.
                                                                                                                                                                                              Hayden MR, Wilson AR, Pimstone SN;
                                                                                                                        (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                 (XENO-) XENON BIORESEARCH INC.
                           99US-0138048.
99US-0139600.
99US-0151977.
       99US-0124702.
                                                                                                                                                                                                                                                                                                                                                                    disease and cancer -
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                         08-JUN-1999;
17-JUN-1999;
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Sequence 7864 BP; 2014 A; 1860 C; 2011 G; 1978 T; 1 other;

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                                 0; Gaps
 16.8%; Score 60; DB 21; Length 7864;
                   0; Indels
            1.1e-19;
      100.0%; Pred. 10. +ive 0; Mismatches
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Matches 60; (
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AAC69385 standard; cDNA; 7864 BP
                                                         AAC69385;
RESULT 20
              AAC69385
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Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; hIgh density lipoprotein;
Tangler disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
cerebrovascular disease; peripheral vascular disease;
Alzheimer's disease; meripheral vascular disease;
X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
                 Human ABC1 cholesterol transporter TD-1 mutant cDNA (T4503C).
                                                                                                                                                                                                                                                         Pimstone SN;
                                                                                                                                                                                                                             (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                     (XENO-) XENON BIORESEARCH INC
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                                                                                                                                                                 15-MAR-2000; 2000WO-IB00532.
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29-JAN-2001 (first entry)
                                                                                                                                                                                                                                                      Hayden MR, Wilson AR,
                                                                                                                                                                                                                                                                       WPI; 2000-587528/55.
                                                                                                                                                                                                                                                                                P-PSDB; AAB38104.
                                                                                                                                WO200055318-A2.
                                                                                                                                                                                    15-MAR-1999;
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New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and cancer -

Examples; Page -; 229pp; English.

The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is coveted on chromosome 9931, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders. Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease.

Conversely, a high level of HDL has protective effects against transcent of the area protective effects against and the area of the area of the area of the area of the area of the area o cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact mano acid sequences of Genbank Accession No: CAAJ10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: The provides of Carolina and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The transgenic cells and non-human animals comprising human AEC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease,

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The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9931, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
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present sequence represents CDNA encoding a mutant human ABC1 cholesterol transporter associated with an altered cholesterol level and therefore an altered risk of carditovascular disease.

Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 cDNA shown on pages 157-160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangler disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
cerebrovascular disease; peripheral vascular disease;
Albachmer's disease; nemipheral vascular disease;
Allachmer's disease; Nemann-Pick disease;
Allachmer's disease; Nemann-Pick disease;
Allachmer's disease; Nemann-Pick disease;
Allachmer's disease; peripheral vascular disease;
prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
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ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ABC1 cholesterol transporter TD-2 mutant cDNA (A1864G).
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                                                                                                                       Sequence 7864 BP; 2014 A; 1861 C; 2011 G; 1977 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                 AAC69386 standard; cDNA; 7864 BP
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are distinguishable in that TD is an autosomal recessive disorder, while CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also crebrovascular disease, particularly coronary artery disease, but also crebrovascular disease.

CC conversely, a high level of HDL has protective effects against transpenic cells and non-human animals comprising human ABC1 nucleic cardiovascular disease. The invention provides genetic constructs and transpenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression compounds which mimic ABC1 activity, compounds which mimic ABC1 activity, compounds which are relates to methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, coronary restences of peripheral vascular disease, muth ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease. Humington's disease, X-linked adrenoleukodystrophy and cancer. Corebrovascular disease, X-linked adrenoleukodystrophy and the nucleic can be invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAAl0005.1 and X75926, and the nucleic can expression no more an invention a mitant human aguine as GenBank Accession No: AD012376.1. The procession accept sequence as GenBank Accession No: AD012376.1. The procession and animal additional activity and animal additional activity and animal additional activity and animal additional activity and animal additional activity and animal additional activity and animal additional activity and animal additionaly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter associated with an altered cholesterol level and therefore an altered risk of cardiovascular disease.
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ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
cerebrovascular disease; peripheral vascular disease;
Albahaner's disease; Homann-Pick disease; Huntington's disease;
X-linked adrenoleukodystrophy, cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7864 BP; 2013 A; 1860 C; 2012 G; 1978 T; 1 other;
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99US-0139600.
99US-0151977.
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Best Local Similarity 100.0
Matches 60; Conservative
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17-JUN-1999;
01-SEP-1999;
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The invention relates to the human ABCI cholesterol transporter protein (183802) and to nucleic acid sequences (C69120) which encode it. ABCI is a member of the APP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly corrections, and plays a crucial role in cholesterol transports, particularly conversed in cholesterol trafficking in monocytes and fibroblasts being involved in cholesterol efflux from the cell. The gene encoding ABCI is involved in cholesterol efflux from the cell. The gene encoding ABCI is involved in cholesterol efflux from the cell. The gene encoding ABCI is involved in cholesterol and familial HDL deficiency (FHA). These discases confloates (TD) and familial HDL deficiency (FHA). These discases confloates (TD) and familial HDL deficiency (FHA). These discases confloates practiced with a high risk of cardiovascular chisease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and cardiovascular disease. The invention provides genetic constructs and cardiovascular disease compounds which mained administration of an expression cardiovascular disease compounds which mained administration of an expression compounds which mained administration of an expression of the encompasses compounds which mained administration of an expression of increased risk for cardiovascular disease, especially coronary arestenosis or peripheral vascular disease, coronary restenosis and be used in the treatment of disease. They may also be used 
                                                                                                                                                                                                                      New ABC1 polypeptide is useful for treating diseases associated with ABC1 blological activity, e.g. Alzheimer's disease, Huntington's
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                                                                                                Hayden MR, Wilson AR, Pimstone SN;
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                         (UYBR-) UNIV BRITISH COLUMBIA.
                                                (XENO-) XENON BIORESEARCH INC.
                                                                                                                                                                                                                                                                      disease and cancer -
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0; Gaps
                  0; Indels
     100.0%; Pred. No. 1.1 cive 0; Mismatches
                                                                                                                             AAS06120 standard; cDNA; 9741 BP.
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Best Local Similarity 100.0
Matches 60, Conservative
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The sequence represents the coding sequence #1 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological mathorics and other and neurological mathorics.
                                                                                                                                                                                                                                                                                                                                                                                                          s M, Arnould-Reguigne I, Prades C, Naudin L,
Jaye M, Searfoss GH, Remaley A, Brewer HB;
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                                            Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease;, LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
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                                                                                                                                                                                 /*tag= a
/product= "Human ABC1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 204-208; 368pp; English.
                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                            26-OCT-2000; 2000WO-EP10886.
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01-MAR-2000; 2000US-0186260.
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                 Human ABC1 DNA sequence #1.
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Best Local Similarity 100.09
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                                                                                                                 Homo sapiens.
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Lemoine C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treatming and preventing ardiovascular and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                      Naudin L;
                                                                                                                                                                                                                                                                                                    Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L
Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9854;
                                                                                                                                                                                                                                                                                                                                                                                                            New human ABC1 nucleic acids and polypeptides for treating atherosclerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                      /product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA clone (5'-primer) SEQ ID NO:4267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 209-213; 368pp; English.
                                                        Location/Qualifiers
298..7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH07432 standard; cDNA; 736 BP
                                                                                                                                                                                              26-OCT-2000; 2000WO-EP10886
                                                                                                                                                                                                                            99EP-0402668
                                                                                                                                                                                                                                       01-MAR-2000; 2000US-0186260
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                                                                                                                                                                                                                                                                          (AVET ) AVENTIS PHARMA SA.
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P-PSDB; AAU02176.
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                                                                                                                                    WO200130848-A2
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                               Homo sapiens
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                                                                                                                                                                                                                             26-OCT-1999;
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                                                                                                                                                                                                                                                                                                    Denefle P,
Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oilgo-dr primer and an oilgonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence of the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also weeful for the full-length cDNAs are primers allow obtaining of the full-length cDNAs represent human cDNA sequences; AAH13629 to AAH13629 to AAH13629 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 consequences.
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                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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                                                                                                                                                                                                         Yamamoto J;
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                                                                                                                                                                                                   Isogai T, Nishikawa T, Hayashi K, Saito K, Ya
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                    claim 1; SEQ ID 4267; 2537pp + CD ROM; English
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                                                  99JP-0248036.
                                                                                        11-JAN-2000; 2000JP-0118776.
              28-JUL-2000; 2000EP-0116126
                                                                                                        02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
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Matches 51; Conserv
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                                                                      27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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Otsuki T;
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100.0%; Pred. No. 2.9e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sogai T, Nishikawa T, Hayashi K, Si
Sugiyama T, Wakamatsu A, Nagai K,
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                                                                                                                                                                                                                                        99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                               28-JUL-2000; 2000EP-0116126
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Matches 51; Conservative
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11-JAN-2000;
02-MAY-2000;
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07-FEB-2001
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The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density ilpoprotean-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABG1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                        Treating a lower than normal high density lipoprotein-cholesterol (HDL-0) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
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Pred. No. 2.1e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37 BP; 4 A; 17 C; 11 G; 5 T; 0 other;
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                                                                                                                                                                                                   Hayden MR, Brooks-Wilson AR, Pimstone SN,
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                                                                                                                                                        (UYBR-) UNIV BRITISH COLUMBIA
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                                                                                                             15-MAR-2000; 2000US-0526193. 23-JUN-2000; 2000US-0213958.
                                                                     01-SEP-2000; 2000WO-IB01492.
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2000US-0213958.
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                                                                                                                                                                       (XENO-) XENON GENETICS INC
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Best Local Similarity 100.0
....hes 35; Conservative
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             WO200115676-A2.
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                                        08-MAR-2001
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W09957145-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ39175;
                                                                                                                                 Lees AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
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                                                                                                                               The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                         Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human low density lipoprotein binding protein 2 (LBP-2) gene.
                                                                                                                                                                                                                                                                                 Length 38;
                                                                                                                                                                                                                                                                                                     0; Indels
                    Pimstone SN, Clee SM;
                                                                                                                                                                                                                                                                               9.8%; Score 35; DB 22; 1 Local Similarity 100.0%; Pred. No. 2.1e-07; Nes 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                  Sequence 38 BP; 6 A; 15 C; 5 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                         78 ccctcctgctttatctttcagttaatgaccagcc 112
                                                                                                                                                                                                                                                                                                                                   1 ccctcctgctttatctttcagttaatgaccagcc 35
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/note= "includes introns"
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2832..5153
/*tag= a
                                                                                                                 Disclosure; Fig 17; 317pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 AAH26495 standard; DNA; 12425 BP.
                     Hayden MR, Brooks-Wilson AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,4502
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4995..5153
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.4694
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3786..4207
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 (XENO-) XENON GENETICS INC
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4208..4
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4594..4
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                                          WPI; 2001-244356/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAH26495;
                                                                                                                                                                                                                                                                                  Query Match
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bone disease; osteolyperplasia; osteometastasis; orthopaedic surgery; osteoarthritis; arthrostatis; tumour dissection; bone reconstruction; spinal fusion; vertebral canal enlargement; congenital cartilage disease; dysoteogenesis; achondroplasia; palatoschisis; mandible reconstruction; residual ridge construction; osteoporosis; morphogenesis; hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of genomic DNA encoding novel human conversity lipoprotein binding protein 2 (LBP-2, see AAB82806).

The DNA was isolated from a human genomic library by screening with LBP-2 bundleic acids are among claimed plane spans 5 exons. Human LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of inding to native and methylated LDL. Also claimed are isolated LBP propeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk con atherosclerosis, methods for treating an agent for use in abnormality in structure or metabolism of LBP are claimed.

The properties of the methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BMP-4 5' upstream gene sequence with exon 1-3 PCR primer #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid, and vaccine compositions, are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Law SW, Arjona AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2395 ggaggagggagggagggaaggaag 2418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 23; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     (BOST-) BOSTON HEART FOUND INC.
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                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000US-0616289.
                                                                                                                                                                                                                         28-FEB-2001; 2001WO-US06356
                                                                                                                                                                                                                                                                                                      02-MAR-2000; 2000US-0517849
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Matches 24; Conservative
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lees RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB82806
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                                                                         WO200164874-A2
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15-MAY-2000; 2000WO-GB01849. 15-MAY-1999; 99GB-0011247.

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molecular weight compounds and their expression of immune ner-q. The molecular weight compounds and their derivatives have morphogenetic activity and inhibiting activity for bone and cartilage through the expression of human BMP-q, and are useful as preventative or therapeutic expression of human BMP-q, and are useful as preventative or therapeutic general construction of steohyperplassia, and as remedies for osteometastas. The compounds are also useful in the fields of orthopaedic surgery (fracture, osteoarthritis such as joint and hip joint osteoarthritis, arthrosteids, damage of cartilage such as damage of meniscus, regeneration of bone and cartilage deficit caused by injury and tumour dissection, bone reconstruction such as spinal cone diseases such as dysoteogenesis and achondroplasia); or dental fields (bone reconstruction such as palatoschisis, mandible ceconstruction, and residual ridge construction) and osteoporosis. The compounds may also be used for bone graft in aesthetic surgery. The compounds also have application in the veterinary field. Those compounds therewer, of home are all and an expression and contention and horse.
                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a PCR primer for the 5' upstream gene sequence including the exon 1 through exon 3 regions of human bone morphogenetic protein 4 (BMP-4). This region of DNA and a reporter gene can be introduced into a host cell, and used to identify low molecular weight compounds which regulate the expression of human BMP-4. The low
                                                                                                                                                                                                                                                                                                   .ow molecular weight compounds which regulate the expression of BMP-4
                                                                                                                                                                                                                                                                               Human bone morphogenetic protein 4 (BMP-4) promoter used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence from the promoter region upstream of the See2a gene #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Senescence; transgenic plant; promoter; transcription initiation; plant development; fruit ripening; protease inhibitor; pesticide; silage proteolysis inhibition; See2a; ds.
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6.2%; Score 22; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy of bone and cartilage hyperplasia.
                                                                                                                                                   (HMRI ) HOECHST MARION ROUSSEL LTD.
                                                                                                                                                                                                                                                                                                                                              Example 1; Page 23; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC83229 standard; DNA; 1077 BP.
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                                                                  99WO-IB00732.
                                                                                                          98JP-0120173
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                                                                                                                                                                                               Kawai S, Sugiura T;
                                                                                                                                                                                                                                       WPI; 2000-062142/05
                                                                22-APR-1999;
                                                                                                        30-APR-1998;
                        11-NOV-1999
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This invention relates to a promoter or transcriptional initiation region of a plant genome that is capable of modifying gene expression during plant material senescence. Plant senescence is the sequence of during plant material senescence. Plant senescence is the sequence of blochemical and physiological events comprising the final stage of plant development. The promoter or a DNA construct containing the promoter is useful for modifying gene expression during senescence, for delaying senescence characteristics, and for modifying the expression of strong also be used for the expression of antisense or senes protease sequences, dataying fruit ripening, enhancing senescence characteristics of plant material, modifying expression of at least 1 plant growth regulator, for transforming plant material with a transgene under the control of the promoter of modifying expression of a protease inhibitor, pesticidal comporter, for modifying expression of at least 1 chemical product gene. The promoter and DNA construct are also useful for producing a plant material having modified gene expression during senescence, and for the expression of pesticidal compounds during senescence, and for the expression of pesticidal compounds during senescence, and for the expression of a producing a plant material having modified gene expression during senescence, and for the expression of pesticidal compounds during senescence, and for the expression of a producing a plant material having modified gene expression during senescence, and for the expression of pesticidal compounds during senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the promoter or a construct containing it. The present sequence represents a second variant of DNA from the promoter region upstream of the senescence-enhanced See2a gene isolated from Zea mays. This sequence
                                                                                                                                                                                                                                                    modification of gene expression during senescence of plant material and for modifying expression of protease inhibitors and pesticidal genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter; bone morphogenetic protein-4; BMP-4; estrogen receptor; osteoporosis; antitumour agent ICII64384; breast cancer; oestrogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                              Promoter or DNA construct isolated from maize, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 22; DB 22; Length 1077; 100.0%; Pred. No. 0.52; Ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1077 BP; 328 A; 255 C; 236 G; 258 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be used as the promoter region of the invention.
                                                                                                                                          Robson PRH, Griffiths CM;
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/note= "Transcription start site"
1442..1456
                                                                                       (GRAS-) INST GRASSLAND & ENVIRONMENTAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Claim 1; Page 63; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1070 GGAGGGAGGGAAGCAAGC 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV32783 standard; DNA; 1456 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BMP-4 promoter region 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1998 (first entry)
                                                                                                                                       Donnison IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Conservative
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                                                                                                                                                                                WPI; 2001-025023/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                       Thomas H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_signal
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Gaps

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23-NOV-2000

91US-0709621. 92US-0856110.

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Claim 1; Column 23-24; 18pp; English
                   05-JUN-1991;
                                         27-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human bone morphogenetic protein-4 promoter (BMP-4) region 1. The invention provides a method for the identification of therapeutic agents for use in the prevention and/or treatment of osteoporosis. The method involves introducing two expression vectors into a host cell. The first expression vector comprises of a BMP-4 promoter region 1 or 2 (AAV32784) which is operably linked to a reporter gene, e.g. BMP-4 gene. The second expression vector comprises of a DNA encoding an estrogen receptor. The host cell is then contacted with the compounds being being tested for therapeutic activity. Compounds which bind and form a complex with the estrogen receptor, to gain entry into the cell, and then induce the expression of the reporter gene, through the BMP-4 promoter region, are potential therapeutic candidates. By this method, the antitumour agent ICII64384 was shown to be an effective therapeutic agent. Unlike oestrogens currently used to treat osteopoxosis, the therapeutic agents are claimed not to have an increment in the risk of developing breast or endometrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Promoter from human bone morphogenetic protein-4 gene - and related vectors and transformed cells, useful for screening agents for the treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 22; DB 19; Length 1456; 100.0%; Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1456 BP; 357 A; 361 C; 410 G; 328 T; 0 other;
                          /note= "Partial intron sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 5a; 41pp; English.
                                                                                                                                                                                                                                                                                                       Dijkema R, Van Den Wijngaard
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                                                                                                                                                                                                             96EP-0203283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.28
Best Local Similarity 100.0
Matches 22; Conservative
       /number= 1
                                                                                                                                                                                                                                                           (ALKU ) AKZO NOBEL NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment; dimer; ss
                                                                                                                                                                                                                                                                                                                                                WPI; 1998-322720/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-1992;
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                                                                                                                                                                  20-NOV-1997;
                                                                                                                                                                                                             22-NOV-1996;
                                                                           WO9823740-A1
                                                                                                                      04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ32853;
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The sequences given in AAQ32850-56 encode bone morphogenetic proteins (BMP). BMP's increase bone growth and when used in conjunction with vitamin D the level of new bone growth is greater than when a BMP or vitamin D are used alone. The BMP's are administered for systemic treatment at a dose range of 1pg to 100 microg. BMP are active as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bone morphogenetic protein; BMP; growth; vitamin D; fracture; arthritis; surgical lesion; periodontal disease; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 22; DB 13; Length 1751;
100.0%; Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation of new bone growth – by co-administering bone morphogenetic protein and vitamin \boldsymbol{D}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                           Synergistic compsn. for generating mammalian bone growth comprises vitamin=D cpd. and bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1751 BP; 394 A; 510 C; 490 G; 357 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bone morphogenetic protein BMP-4 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.2%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.5 Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                        Disclosure; Page 31-32; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 ggaggaggaggaggaagga 347
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92US-0856110.
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95US-0377292
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(PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1998 (first entry)
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13-MAY-1994;
23-JAN-1995;
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27-MAR-1992;
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                                                    Stone RL;
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mammal. The method comprises administering a bone morphogenetic protein in combination with a vitamin D compound, where: (a) the bone morphogenetic protein is BMP-2 and is administered in an amount of 500-1000 ng in combination with about 6 ng vitamin D compound; or (b) the bone morphogenetic protein is BMP-4 and is administered in an amount of about 62.5 ng in combination with about 6 ng vitamin D compound. The present sequence encodes BMP-4. The method is used for treating bone defects or disorders, e.g. fractures, surgical lesions, periodontal disease, osteoporosis, arthritis and rickets.
                                                                                                                                                                                                                 Gaps
           new method has been developed for generating new bone growth in a
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                                                                                                                                                                                   Score 22; DB 19; Length 1751;
; Pred. No. 0.52;
0; Mismatches 0; Indels (
                                                                                                                                             Sequence 1751 BP; 394 A; 510 C; 490 G; 357 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pang RHL;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence encoding osteogenic protein CBMP2B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     AAQ53144 standard; cDNA; 1788 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= CBMP2B
                                                                                                                                                                                                                               Oppermann H,
                                                                                                                                                                                  Query Match 6.2%;
Best Local Similarity 100.0%;
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91US-0810560.
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                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1994 (first entry)
                                                                                                                                                                                                            22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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18-OCT-1990;
18-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5266683-A.
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17-0CT-1989;
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20-AUG-1990;
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04-DEC-1990;
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23-FEB-1989
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                                                                                                                                                                                                            Matches
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Gaps
                                                       The osteogenic protein when in association with a matrix can induce at the locus of an implant the full development cascade of endochodraal bone formation including vascularisation, mineralisation and bone marrow differentiation. The osteogenic protein can also be used to repair both bone and cartilage in the treatment of osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                               Prepro human CBMP2B; cartilage and endochondrial bone formation; allograft repair; osteoarthritis; non-union fracture repair; osteogenesis; periodontal, dental and craniofacial reconstruction;
                                                                                                                                                                                                      ö
New pure mammalian osteogenic proteins – induce cartilage and endochondral bone formation when in association with a matrix
                                                                                                                                                                           6.2%; Score 22; DB 14; Length 1788;
100.0%; Pred. No. 0.52;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                    0.52;
has 0; Indels
                                                                                                                                         Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
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                               Claim 37; Columns 93-96; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
403..1629
                                                                                                                                                                                                                                                                                                       AAQ72710 standard; cDNA; 1788 BP
                                                                                                                                                                                                                        326 ggaggagggagggagga 347
                                                                                                                                                                                                                                              15 ggaggagggagggaggga 36
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880S-0232630.
890S-0422613.
890S-0422693.
900S-0483913.
900S-0569920.
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90US-0621988.
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90US-0841646.
90US-0993387.
                                                                                                                                                             Query Match
Best Local Similarity 100.vv
Best Local 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Prepro human CBMP2B cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-1989;
22-FEB-1990;
20-AUG-1990;
07-SEP-1990;
18-OCT-1990;
18-OCT-1990;
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04-DEC-1990;
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Homo sapiens
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                            04-DEC-1990;
04-DEC-1990;
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28-JAN-1992;
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         18-OCT-1990;
                   21-NOV-1990;
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                     AAQ72710 encodes AAR51654 prepro human CBMP2B, fragments of the related protein CBMP3 (AAR51642) consisting of residues 93-109 and 77-83 are uniglycosylated osteogenic polyeptides. These polypeptides can be disulphide bonded to form a dimer, which forms an essential in a biodegradable matrix which can be implanted into a mammalian bone marrow cavity, here it can induce local cartilage, bone and endochondrial bone formation; and it can also accelerate allograft repair. This implant has the advantage of inducing all stages of bone formation and of having a higher specific activity than other known biosynthetic materials. The implant can be used to repair non-union fractures and cartilage; treat osteoarthritis; and aid
                                                                                                                                                                                                                                                                                                                     ;
0
                                        Implantable device for inducing osteogenesis - comprises porous matrix contg. non-glycosylated dimeric, di:sulphide linked osteogenic protein.
                                                                                                                                                                                                                                                                                              6.2%; Score 22; DB 15; Length 1788; 100.0%; Pred. No. 0.52; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        in periodontal, dental or craniofacial reconstruction.
                                                                                                                                                                                                                                                               Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
                                                                                    Disclosure; Columns 91-96; 128pp; English
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/product= Prepro-CBMP2B
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAT02601 standard; cDNA; 1788 BP
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890S-0422613.
890S-0422699.
900S-0483913.
900S-0569920.
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88US-0232630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403..1629
                                                                                                                                                                                                                                                                                               Query Match 6.2
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CBMP2(b) cDNA.
        WPI; 1994-324521/40.
                    P-PSDB; AAR51654
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22-FEB-1990;
20-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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15-AUG-1988
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                            AAT02601
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The sequences given in Antonous Library and partial sequence of CBMP3. These proteins, CBMP2B and the partial sequence of CBMP3. These proteins have true osteogenic activity when properly folded and dimerised. CBMP2B and CBMP2A may form a heterodimer with mature hop-1. These proteins contain a conserved six or seven cysteine skeleton in their active regions. Probes based on this region have been used in the solution of further osteogenic protein family members. Fragments of these proteins can be used in the production of dimeric peptides which may be used in the generation of antibodies with binding specificities for osteogenic proteins. The antibodies with binding specificities for osteogenic proteins. The antibodies with binding specificative specifically to an epitope of the osteogenic protein and may be used in purification protocols. Osteogenic proteins, such as these, may be used in an implantable osteogenic device which allows predictable bone in an implantable osteogenic device which allows predictable bone formation correct acquired and congenital cranôferial and other skeletal or dental anomalies. They may be used to induce local endochrondral bone formation in non-union fractures and in other clinical applications including dental and periodontal applications where bone formation is required. Other potential applications including certain of protein applications including certain of protein applications including certain of protein applications include carfilage repair, e.g. in the treatment of osteoarthritis. This sequence was repair, e.g. in the breatment of osteoarthrities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies with osteogenic protein binding specificity - used in purification of osteogenic proteins, and as antigenic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; osteogenic protein; subunit; endochondral bone formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAT02601-03 encodes the human osteogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozkaynak E, Rueger DC;
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Best Local Similarity 100.0%; Pred. No. v..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 93-96; 129pp; English
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403..1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuberasampath T, Oppermann H,
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900S-059543.
900S-0616374.
900S-0621849.
900S-0621889.
910S-0660162.
910S-0810560.
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Chondrogenic protein; biodegradable matrix; cell proliferation; cell differentiation; migratory progenitor cell; cartilage formation; allogenic implant; xenogenic implant; endochondral bone formation; osteogenic protein; CBMP2; ss.

Homo sapiens

US5958441-A. 28-SEP-1999 88US-0179406. 88US-0232630. 92US-0841646. 89US-0422699. 90US-0621988.

08-APR-1988; 15-AUG-1988; 21-FEB-1992;

24-MAY-1995;

91US-0660162 93US-0147023 89US-0315342

17-OCT-1989; 04-DEC-1990; 22-FEB-1991; 01-NOV-1993; 23-FEB-1989; 17-OCT-1989;

90US-0569920 90US-0599543 90US-0616374 90US-0621849 91US-0810560

22-FEB-1990; 20-AUG-1990; 07-SEP-1990;

18-OCT-1990; 18-0CT-1990 21-NOV-1990 04-DEC-1990 20-DEC-1991 28-JAN-1992

89US-0422613 90US-0483913

Human prepro CBMP2B coding sequence.

(first entry)

16-DEC-1999

AAZ27580;

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The present sequence encodes a human osteogenic protein, which is used in the present invention. The present invention describes methods for selectively extracting an osteogenic protein (OP) from a mixture. The method comprises: (a) exposing the mixture to an antibody that specifically binds OP, separating the resulting antibody-protein complex from the mixture, and dissociating the complex. In the methods OP comprises a pair of oxidised subunits that are disulphide-bonded to form a dimer, and one of the subunits has an amino acid (aa) sequence sufficiently homologous to residues 335-431 of a 431 aa protein designated OPS, sequence given in the specification. In dimeric form OP is capable of inducing cartilage and endochondral bone formation in a mammal when disposed within a matrix implanted in the mammal. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extraction of osteogenic protein from mixture - using antibodies specific for novel polypeptide chains useful as subunit(s) of dimeric osteogenic protein(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL;
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/function= "Osteogenic protein"
/product= "CBMP2B"
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18-OCT-1990;
21-NOV-1990;
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22-FEB-1990;
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                                                                   03-FEB-1998
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22-FEB-1
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28-JAN-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Implant for mammals permitting the influx, proliferation and differentiation of migratory progenitor cells, useful for inducing endochondral bone formation in mammals -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 20; Length 1788; Pred. No. 0.52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes the human CBMP2B protein.
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Best Local Similarity 100.0%; P.
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Query Match

326 ggaggaggagggaggaagga 347  AAZ27580 standard; cDNA; 1788 BP.

RESULT 39 AAZ27580 ID AAZ2

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6.2%; Score 22; DB 19; Length 1788; 00.0%; Pred. No. 0.52;

Rueger DC, Pang RHL, Kuberasampath T, Ozkaynak E, Oppermann H;

(STYC ) STRYKER BIOTECH CORP.

WPI; 1999-589530/50. P-PSDB; AAY43112. Page 23

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RESULT

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The present invention describes isolated DNA (I) encoding at least one osteogenically active region of human osteogenic protein-1 in prepro form (OP1-PP), murine OP2-PP or human OP2-PP. Also described are: (A) DNA related to (I) encoding a polypeptide able to form dimers that can induce cartilage and endochondral bone formation in a mammal when implanted in a matrix; (B) vectors containing (I) or related DNA; (C) host cells transformed with this vector; (D) DNA (I) encoding a prepro- or pro-OP1, and related vectors and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding mammalian osteogenic proteins in prepro form - able to induce cartilage and bone formation when implanted in matrix, useful for repairing bone defects
                                                                                                          Human; osteogenic protein; OP-1; OPX; endochondral bone formation; cartilage; craniofacial defect; skeletal disorder; dental disorder; non-union fracture; osteoarthritis; vascularisation; mineralisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL;
                                                                                                                                                                                                                                               "osteogenic protein"
                                                                                    Human osteogenic protein CBMP2B encoding cDNA
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                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                        /product= "CBMP2B
          AAX00232 standard; cDNA; 1788 BP
                                                                                                                                                      bone marrow differentiation; ss.
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91US-0810560.
92US-0827052.
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9005-0616374.
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88US-0232630.
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                                                             (first entry)
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20-AUG-1990;
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18-OCT-1990;
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01-NOV-1993
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AAX00232
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mammalian cells, able to induce bone and cartilage formation; (F) mature opt secreted from mammalian cells following expression of the sequence that encodes hoPl-PP; and (G) production of an active osteogenic composition by truncating mature opl protein. Host cells of (C) are used to produce proteins able to induce cartilage and bone formation, e.g. for correction of acquired or congenital craniofacial defects or other skeletal or dental disorders; to heal non-union fractures; to repair cartilage, e.g. in osteoarthritis, or generally wherever bone formation is required. The proteins induce complete development of endochondral bone, including vascularisation, mineralisation and bone marrow differentiation. The present sequence encodes human CBMP2B.
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                                                                                                                                                                                                                                                                                                                    6.2%; Score 22; DB 20; Length 1788;
100.0%; Pred. No. 0.52;
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                                                                                                                                                                                                                                                             Sequence 1788 BP; 418 A; 515 C; 494 G; 361 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #15183.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS79379 standard; cDNA; 1832 BP
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                            Query Match
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imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. AAS641954 represent novel human lagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       bone morphogenic protein; BMP 2B; cartilage; periodontal disease;
tissue repair; osteoporosis; treatment; oligonucleotide probe; ss.
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/note= "BWP-2B contains at least this part of the
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                                                                                                                                                                                               DB 23; Length 1832; 0.52;
                                                                                                                                                                                                                        0; Indels
                                                                                                                                                      Sequence 1832 BP; 447 A; 439 C; 432 G; 484 T; 30 other;
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/product= Bone-morphogenic_protein_2B
1333..1626
                                                                                                                                                                                    6.2%; Scor.
100.0%; Pred. No. v...
                                                                                                                                                                                                                                                                                                                                                                                                               Human bone morphogenic protein (BMP) 2B cDNA.
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                                                                                                                                                                                                                                                                      1321 AGGAGGGAGGGAGGAAG 1300
                                                                                                                                                                                                                                                                                                                                    AAT78942 standard; cDNA; 1944 BP.
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87US-0028285.
88US-0179100.
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403..1629
                                                                                                                                                                                                                     22; Conservative
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                                                                                                                                                                                                         Local Similarity
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P-PSDB; AAW24850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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07-SEP-1993;
01-JUL-1986;
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                                                                                                                                                                                             Query Match
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5'UTR
                                                                                                                                                                                                                                                                                                           RESULT 42
                                                                                                                                                                                                                     Matches
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The HindIII-SacI bovine genomic bBMP-2 fragment described in AAN80627 is subcloned into M13, labelled and used as probe to screen polyadenylated RNAs from various cells and tissue sources.
Sequence analysis of the weakly hybridising recombinants hBMP-2 class II (-BMP-4) indicated that they are quite homologous with the sequence given in AAN80622 at the end of their coding regions, but less so in
                                                                                                     This cDNA sequence encodes the human bone morphogenic protein (BMP) 2B. Oligonucleotide probes were synthesised based on a partially sequenced BMP-2B protein isolated from ground bowine powder. The probes were used to screen a bowine liver DNA library to obtain the BMP-2B encoding DNA sequence. The DNA was used to screen a U-2 OS human cell line cDNA library to obtain this human BMP-2B cDNA. BMPs can be used to induce bone and cartilage formation, and in wound healing and tissue repair. They can also be used for treating periodontal disease or osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bone morphogenic protein; hBMP-2 class II; probes; cartilage formation; bone formation; osteogenic cpds; prodontal disease; ss.
                                                                                                                                                                                                                                                                                                                                                            Gaps
Production of human bone morphogenic protein 2A or 2B in cell culture - useful inducing bone or cartilage production, in wound healing and tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bone morphogenic proteins - obtd. using recombinant DNA and used for inducing cartilage and bone formation.
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                                                                                                                                                                                                                                                                                                                  1 6.2%; Score 22; DB 18; Length 1944; Similarity 100.0%; Pred. No. 0.52; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Bone Morphogenic Protein-2 class II cDNA from U2OS-3.
                                                                                                                                                                                                                                                                  Sequence 1944 BP; 488 A; 535 C; 510 G; 411 T; 0 other;
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                                                                      Example 5; Fig 3; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                      326 ggaggaggaggaagga 347
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                                                                                                                                                                                                                                                                                                                                                     22; Conservative
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Best Local S
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bone fractures; improved fixation of artificial joints; in cosmetic plastic surgery; and in treatment of periodontal disease, burns,
                                             incisions, ulcers etc.
See also AAQ14035 and AAQ14036, AAQ14909 and AAQ14910.
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                                                                                                                                                                                                                                                               326 ggaggagggagggagggagga 347
                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ31870 standard; DNA; 1954 BP
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                                                                                                                                                                                                                                                                                                        15 ggaggagggagggaagga 36
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87US-0028285.
88US-0179100.
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Best Local Similarity 100.C
Matches 22; Conservative
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20-MAR-1987;
08-APR-1988;
11-JUL-1989;
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                           Human cDNA hBMP-2 class II contains an opem reading frame of 1224 bp, encoding a protein of 408 amino acids. The protein is preceded by a 5' untranslated region of 394 bp with stop codons in all frames, and contains a 3' untranslate dregion of 308 bp following the in-frame stop codon. The 8 bp region preceding this 5' untranslated region represents a linker used in the cDNA cloning procedures. See also AAN80619-N80636 and AAN81963-64.
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                    6.2%; Score 22; DB 9; Length 1954; 100.0%; Pred. No. 0.52; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                      Sequence 1954 BP; 492 A; 536 C; 511 G; 415 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bone; cartilage; osteoinductive protein; ss.
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/label= claim 1(c)
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                                                                                                                                                                                                                                                                                                                                                             326 ggaggagggagggaggga 347
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P-PSDB; AAR14242.
                  the more 5' regions
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                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bone Morphogenic Protein; bacteriophage lambda U2OS-3; ATCC 40342; bone fracture; cartilage defect; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding osteo-inductive proteins - used for producing BMP-2A and BMP-2B for inducing bone or cartilage formation and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "nucleotides 1-8 are from cloning vector"
1627..1954
/*tag= c
                                                                                                                                               ;
0
                                                                                    DB 12; Length 1954; 0.52;
                                                                                                                                                  0; Indels
Sequence 1954 BP; 493 A; 536 C; 511 G; 414 T; 0 other;
                                                                                       6.2%; Score 22; DB 100.0%; Pred. No. 0.5 Live 0; Mismatches
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/product= pre-pro-BMP-2B
9..402
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Search completed: September 20, 2002, 06:07:38 Job time: 10342 sec

45, Appl 8, Appli 7, Appli

Sequence Sequence Sequence

, Appl , Appl Appli

Sequence 13, Sequence 13,

Appli Appli Appli Appli Appli Appli Appli

Sequence 1, P Sequence 1, P Sequence 7, P Sequence 4, P Sequence 1, P

US-09-211-710-9 US-08-975-316-45 US-08-705-71-8 US-09-370-807-7 US-09-370-807-7 US-09-173-914-1 US-09-173-914-1 US-08-483-376-1 US-08-483-376-1 US-08-460-895-7 US-08-460-895-1 US-09-210-889-1 US-08-69-7 US-08-69-1-889-1 US-08-69-1-889-1 US-08-69-1-889-1 US-08-69-1-889-1 US-08-69-1-889-1 US-08-69-1-889-1 US-08-69-1-889-1 US-08-69-1-889-1 US-08-69-1-889-1

624 624 1344 2407 2419 2419 6078 6386 35060 31634

0 0 0 0 0 0 0 0 0

Sequence 3, P Sequence 14,

US-09-078-294-4 US-09-078-294-3 US-09-109-663-14

1649 1649 80246 80595

ALIGNMENTS

Sequence 4, Sequence 1, Sequence 8, Sequence 8,

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Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
                                                                                                                                                                                            (without alignments)
786.045 Million cell updates/sec
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                                                                                                                                                               September 20, 2002, 06:14:47; Search time 111.56 Seconds
                                                                                                                                                                                                                                                                                                                                    1 tggaggtctcagctgagagg.........gagggaaggaagctgtgttg 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-07-901-703-18

US-08-147-023-6

US-08-147-570-6

US-08-449-700-6

US-08-449-699A-6

PCT-US93-05446-18

US-08-050-132A-3

US-08-050-132A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                               OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                     US-09-846-456-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Score Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                        OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                              Run on:
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В
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Substant in Court.

APPLICANT: Dijkema, Rein
APPLICANT: van den Wijngaard, Arthur
TITLE OF INVENTION: Method and materials for the screening of therapeutic
TITLE OF INVENTION: agents for the prevention and/or treatment of
TITLE OF INVENTION: agents for the prevention and/or treatment of
TITLE OF INVENTION: agents for the prevention and/or treatment of
TITLE OF INVENTION: osteoporosis
TITLE OF INVENTION: osteoporosis
TITLE OF INVENTION: osteoporosis
CURRENT PERERROR : 1/96/27 US
CURRENT FILING DATE: 1/99-06-21
EARLIER APPLICATION NUMBER: PCT/REP97/06668
EARLIER APPLICATION NUMBER: EP96203283.5
EARLIER FILING DATE: 1/997-11-20
SARLIER FILING DATE: 1/996-11-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08377292;
Patent No. 5693615
GENERAL INFORMATION:
APPLICANT: STONE, ROGER L.
TITLE OF INVENTION: THERAPEUTIC FORMULAS FOR OSTEOINDUCTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Procter & Gamble Company
STREET: 11810 East Miami River Road
CTTY: Cincinnati
STATE: Ohlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 22; DB 3; Length 1456; 100.0%; Pred. No. 0.053; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1187 ggaggaggagggagggaagga 1208
US-09-308-406-1
; Sequence 1, Application US/09308406
; Patent No. 6159696
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 45239-8707
                                                                                      ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: human
US-09-308-406-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-08-377-292-4
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Sequence 22, Appl Sequence 9, Appli

Sequence 42, P Sequence 7, Ap Sequence 27, P Sequence 22, P

5166058-5 US-08-332-766A-16 US-08-332-766A-17 US-08-332-766A-42 US-09-268-992-7 US-08-332-766A-27 US-08-332-766A-22 US-08-713-000-9

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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
6.2%; Score 22; DB 1; Length 1751;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,292
FILING DATE: 23-JAN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSTEOGENIC DEVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OPPERMANN, HERNANN
APPLICANT: OPPERMANN, HERNANN
APPLICANT: OPRERASAMPATH, THANGAVEL
APPLICANT: RUBEERS, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: PANG, ROY H.L.
APPLICANT: PANG, ROY H.L.
APPLICANT: SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/243,435
FILLIG DATE:
APPLICATION NUMBER: US/08/117,367
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
                                                                                                                                                                                                                                                                                                                                          NAME: COTStanje, Brahm J.
REGISTRATION UNDRER: 34,804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-245-2858
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGHH: 1751 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-377-292-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOSTON
                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-07-841-646-6
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6.2%; Score 22; DB 1; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2B"
/evidence= EXPERIMENTAL
/note= "CBMP2B (CDNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRP-001CP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 403..1626
IDENTIFICATION METHOD: experimental
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 600,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION NUMBER: US 179,460
FILING DATE: O8-ARR-1988
ATTORNEY/AGANTALION:
                                                                                                                                                                                                                                                                                          FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 59, 543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579, 865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
APPLICATION NUMBER: US 569,920
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: PITCHER, EDMUND R. REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION: TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1788 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION:
; OTHER INFORMATION:
US-07-841-646-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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Gaps

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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: RUEGER, DAVID C
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: OPERMANN, HERMANN
APPLICANT: OZAKAYNAK, ENGIN
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: /function= "OSTEOGENIC PROTEIN";
CTHER INFORMATION: /function= "OSTEOGENIC PROTEIN";
CTHER INFORMATION: /forduct= "BMP2B"
CTHER INFORMATION: /forte= "BMP2B (CDNA)"
US-07-901-703-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/901,703

FILING DATE: 19920616

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PITCHER ESQ, EDMUND R

REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: STK-057

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/248-7000

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

FERGURAL TARRES DATES:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: EXCHANGE PLACE, 53 STATE STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          Sequence 18, Application US/07901703
Patent No. 5344654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 ggaggagggagggagggagga 347
15 GGAGGAGGGAGGGAGGA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1788 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JUPULOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02109
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                                                                                                                    RESULT 4
US-07-901-703-18
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US-08-147-023-6
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COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
                                                                              APPLICANT: OPPERMANN, HERMANN
APPLICANT: OXFANANK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
ATILLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US.08/147,023
CLASSIPECATION NUMBER: US.08/147,023
CLASSIPECATION NUMBER: US.08/147,023
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.05/06/191
PRIOR APPLICATION NUMBER: US.05/06/162
FILING DATE: 28-788-1991
PRIOR APPLICATION NUMBER: US.06/162
FILING DATE: APPLICATION NUMBER: US.06/162
FILING DATE: Q4-DEC-1990
PRIOR APPLICATION NUMBER: US.06/198
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US.06/198
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US.06/198
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US.06/07-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.06/024
FILING DATE: 11-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.06/024
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US.06/024
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PRICATION NUMBER: US 579,865
PRICATION NUMBER: US 579,865
PRICATION NUMBER: US 569,920
PRICATION NUMBER: US 569,920
PRICATION NUMBER: US 569,920
PRICATION NUMBER: US 483,913
PRICATION NUMBER: US 483,913
PRICATION NUMBER: US 483,913
PRICATION NUMBER: US 483,913
PRICATION NUMBER: US 483,913
PRICATION NUMBER: US 483,913
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FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 179,460 ELLING DATE: 08.APR-1988 ATTORNEY/AGENT INFORMATION: NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US 599,543
18-OCT-1990
Sequence 6, Application US/08147023 Patent No. 5468845 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
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326 ggaggagggagggagga 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.2%; Score 22; DB 1; Length 1788; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Appellment "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /function="CBMP2B"
US-08-147-023-6

US-08-147-023-6
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: OPPERMANN HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: WIBERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                 REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
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REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GGAGGAGGGAGGGAAGGA 36
                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MASSACHUSETTS
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 403..1626
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APPLICATION NUMBER: U
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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US-08-447-570-6
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Gaps
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/product= "CAMP12B"
/evidence= EXPERIMENTAL
/note= "CBMP2B (CDNA)"
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IDENTIFICATION METHOD: experimental
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTONEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEE-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
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FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
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TELECOMMUNICATION INFORMATION:
TELEFONE:
TELEFONE:
TELEFONE:
TELEFONE:
TELEFONE:
TELEFONE:
TELEFONE:
TENERATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDENESS: single
22-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: HIPPOCAMPUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403..1626
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; OTHER INFORMATION:
US-08-447-570-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMC
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24 MAY-1995 CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993 δy 15 GGAGGGGGGGGGGGGAGGA 36

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Gaps
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Patent No. 593841

GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUBERS, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESCED:
ADDRESCE
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Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 22; Conservative 0; Mismatches 0; Indels
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JEDYTIFLOATION METHOD: experimental
IDBYTIFLOATION FTHOD: Alloction="OSTBOGENIC PROTEIN"
OTHER INFORMATION: /function="CBMP2B"
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /evidence=EXPERIMENTAL
US-08-449-700.6
US-08-449-700.6
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STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                              CRP-001CP6
                                   APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMNUD R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 ggaggagggagggaggga 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MASSACHUSETTS COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 125 H
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110
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US-08-449-699A-6
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DROSTHETIC DEVICES HAVING ENHANCED TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
STREET: 35 South Street
CITY: Hopkinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 403..1626
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="CSPEGGENIC PROTEIN"
OTHER INFORMATION: /product="CBMP2B"
OTHER INFORMATION: /evidence="EXPERIMENTAL
OTHER INFORMATION: /note="CBMP2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US93/05446
           REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 37,829
REFERENCE/DOCKET NUMBER: STK-001CP6CN
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/248-7000
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 ggaggaggaggaggaagga 347
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI: SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19930608 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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ZIP: 01748
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PCT-US93-05446-18
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Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                        NAME/KEY: CDS
| NAME/KEY: CDS
| LOCATION: 403.1626
| IDENTIFICATION METHOD: experimental
| OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
| OTHER INFORMATION: /product= "BMPISH"
| OTHER INFORMATION: /evidence= EXPERIMENTAL
| OTHER INFORMATION: /note= "BMPISH (CDNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wozney, John M.
APPLICANT: Welste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
WUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,132A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteosarcoma Cell Line
U-20S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/08050132A; Patent No. 5661007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 ggaggagggagggaggaagga 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING EVERNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GGAGGAGGGAGGGAAGGA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                              TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                           HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                  MOLECULE TYPE: CDNA HYPOTHETICAL: NO
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02140
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Indels

Pred. No. 0.053; mismatches 0;

Best Local Similarity 100.0%; P. Matches 22; Conservative 0;

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APPLICANT: Wolfman, Neil M.
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.2%; Score 22; DB 1; Length 1954; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Legal Affairs, Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KAPINOS, BILEN J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: G1-5192B
TELEPHONE: 617-876-1170
TELEPHONE: 617-876-1170
TELEFAX: 617-876-1851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARRATERISTICS:
LENGTH: 1954 base pairs
IMMEDIATE SOURCE:
LIBRARY: U20S CDNA in Lambda gtl0
LIONE: Lambda U20S-3
POSITION IN GENOME:
UNITS: bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/07989847
Patent No. 5866364
GENERAL INFORMATION:
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                                                                                                                                                                                                NAME/KEY: mat_peptide LOCATION: 1279..1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                            NAME/KEY: CDS
LOCATION: 403..1629
FEATURE:
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                                                                                                                                                                                                                                                             NAME/KEY: mRNA
LOCATION: 9..1934
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ZIP: 02140-2387
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COCATION:

US-07-989-847-3
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                                                                                                            FEATURE
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DB 2; Length 1954;

6.2%; Score 22;

Query Match

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Rozney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Coleste, Anthony J.
APPLICANT: Coleste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Coleste, Anthony J.
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 19
CORRESPONDENCES: 10
CONTRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTWO - A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bum PC compatible
COMPUTER: Bum PC compatible
COMPUTER: Bum PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC.1996
CLASSIFICATION NUMBER: 08/254,353
FILING DATE:
ATPORNEY/AGENT INFORMATION:
ATPORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,245
REGISTRATION NUMBER: 32,245
REGISTRATION NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENTH: 1954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: U2OS CDNA in Lambda gt10
CLONE: Lambda U2OS-3
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
                                                                                                                                                     Sequence 3, Application US/08750222A Patent No. 6034061
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403..1629
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LOCATION:
FEATURE:
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LOCATION:
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                                                                                                           RESULT 12
US-08-750-222A-3
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Gaps
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                                                          Query Match 6.2%; Score 22; DB 3; Length 1954; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/721,847A

FILING DATE: 14-JUN-1991

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Rapinos, Ellen J.

RECISTRATION NUMBER: 31,245

REFERENCE/DOCKET NUMBER: 5160C

TELEPHONE: 617-876-1170

TELEPHONE: 617-876-5811

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wang,
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Wozney, John M.
TITLE OF INVENTION: No. 6150328el BMP Products
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: U2OS CDNA in Lambda gtl0
CLONE: Lambda U2OS-3
POSTITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/07721847A; Patent No. 6150328
                                                                                                                                              326 ggaggagggagggaggga 347
                                                                                                                                                                       15 GGAGGAGGGAGGGAAGGA 36
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1954 base pairs.
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OKGANISM: Homo Sapiens
IMMEDIATE SOURCE:
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9..1934
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ORGANISM: HOM
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    US-08-815-652B-3
                                                                                                                                                                                                                                                 RESULT 14
US-07-721-847A-5
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FEATURE:
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US-07-721-847A-5
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                                                          Query Match
6:2%; Score 22; DB 3; Length 1954;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,652B
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Thies, R. Scott
TILLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REELEKNICE/DOCKET NUMBER: GI 5186D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: U20S CDNA in Lambda gt10
CLONE: Lambda U20S-3
POSITION IN GENOME:
UNITS: bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08815652B Patent No. 6034062
                                                                                                                                          326 ggaggaggaggaggaagga 347
                                                                                                                                                               15 GGAGGAGGGAGGGAAGGA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide LOCATION: 1279..1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 403..1629
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9..1934
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ORIGINAL SOURCE:
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LOCATION:
                                                                                                                                                                                                                                          RESULT 13
US-08-815-652B-3
US-08-750-222A-3
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TITLE OF INVENTION: No. 6245889el BMP Products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 ggaggagggagggaggga 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GGAGGAGGGAGGGAAGGA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1954 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                         ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
403..1629
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9..1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \frac{9}{2}
                                                                                                                                      COUNTRY: USA ZIP: 02140
                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-925-779-5
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US-08-254-353A-3
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                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Wolfman, Neil M.
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
Heterodimers, Compositions and Methods of Use.
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                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
      Length 1954;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:

NAME: Kapinos, Ellen J.

REGISTATION NUMBER: 32,245

REFERENCE/DOCKET NUMBER: GI-5192B-CON

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-498-8622

TELEPHONE: 617-498-8622

TELEPHONE: 617-4976-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
    Ouery Match 6.2%; Score 22; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 22; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/469,411
FILING DATE: 06-Jun-1995
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 403..1626
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08925779
Patent No. 6245889
GENERAL INFORMATION:
APPLICANT: Wang, Elizabeth A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                   RESULT 15
US-08-469-411-3
; Sequence 3, Application US/08469411
; Patent No. 6190880
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                                                                                 15 GGAGGAGGGAGGGAGGA 36
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA ZIP: 02140-2387 COMPUTER READABLE FORM: MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEOUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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100.0%; Pred. No. 0.053;
tive 0; Mismatches 0; Indels
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
STREET: APT CAMBRIDGEPARK DRIVE
CITY: CANBRIDGE
STATE: MA
                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: U2OS CDNA in Lambda gt10
LICHNE: Lambda U2OS-3
POSITION IN GENOME:
UNITS: bp
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,779
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5160C
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNET/AGENT INPORMATION:
NAME: Kapinos, Ellan J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 5160C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: CDS
LOCATION: 403..1629
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; LOCATION: 9..1934
PCT-US92-05374A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CD
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                   STATE: MA
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                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                                                    ZUMATION 102240
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENTE Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,353A
                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECHMONICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
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GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-20S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: U2OS CDNA in Lambda gt10
CLONE: Lambda U2OS-3
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MOLECULE TYPE: CDNA to MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
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LOCATION: 403.,1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: mRNA
; LOCATION: 9..1934
US-08-254-353A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME:
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PCT-US92-05374A-3
                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                            6.2%; Score 22; DB 6; Length 195
100.0%; Pred. No. 0.053;
ative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/332,766A FILING DATE: 01-NOV-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217211/M94/0434/GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
CORRESPONDENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D. C. COUNTRY: U.S.A. ZIP: 20005-3918
COMPUTER READABLE FORM: MEDIUM TYPE: F. LOPPPY disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-332-766A-16/c; Sequence 16, Application US/08332766A; Patent No. 5843647; Patent No. 5843647; GENERAL INFORMATION:
        APPLICATION NUMBER: 28,285
FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 943,332
FILING DATE: 17-DEC-1986
APPLICATION NUMBER: 880,776
FILING DATE: 01-JUL-1986
SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                     326 ggaggaggaggaggaagga 347
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REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 861-3000
TELEFAX: (202) 882-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-332-766A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 445 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                   Query Match 6.2%
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                              LENGTH: 1954
                                                                                                                                                                                    5166058-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1954;
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                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07084
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.2%; Score 22; DB 5; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 22; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                    GI 5186C-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/378,537
FILING DATE: 11-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 179,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE: Osteosarcoma Cell Line CELL LINE: U-20S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : U2OS cDNA in Lambda gt10
Lambda U2OS-3
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION:
ATTORREY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1210
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 ggaggagggagggagggaagga 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
1279..1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                      02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
PCT-US95-07084-3
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
5166058-5
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SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION NATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATPCHNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
RECISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 20,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New YORK AVenue, N.W.
                                                                                                                                                                                                                                                                                              CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                  RESULT 22
US-08-332-766A-17/c
; Sequence 17, Application US/08332766A
; Patent No. 5843647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/08332766A
Sequence 42, Application US/08332766A
Patent No. 5843647
GENERAL INFORMATION:
340 GGAGGGAGGGAGGAAG 320
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TELERX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                         CITY: Washin
STATE: D. C.
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APPLICANT: Chen, H.

APPLICANT: Freimer, N.

TITLE OF INVENTION: AMETHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AMD TREATING CHROMOSOME-18P RELATED DISORDERS;
FILE REFERENCE: 7883-138

CURRENT APPLICATION NUMBER: 05/236,134

EARLIER APPLICATION NUMBER: 09/236,134

EARLIER PILING DATE: 1999-01-22

EARLIER PILING DATE: 1999-10-28

EARLIER FILING DATE: 1998-10-28

EARLIER FILING DATE: 1998-01-28

EARLIER FILING DATE: 1998-01-28

EARLIER FILING DATE: 1998-01-36

EARLIER FILING DATE: 1998-01-36

EARLIER FILING DATE: 1998-01-66

SARLIER FILING DATE: 1998-01-66

EARLIER FILING DATE: 1998-01-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: U1-NOV-1994
CLASSIFICATION: 432
PRICASIFICATION: 438.
PRICATION: DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/09268992
; Patent No. 6342351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 861-3000
TELEPAX: (202) 862-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-332-766A-42
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5.6%; Score 20; DB 4; Length 72604; 100.0%; Pred. No. 0.58; tive 0; Mismatches 0; Indels (
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                                           0; Indels
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REGISTRATION NUMBER: 5,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217211/M94/0434/GB
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUN, John
TITLE ANNOTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 New York Avenue, N.W.
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                                                                                                                                                                                                                                  Sequence 27, Application US/08332766A
Patent No. 5843647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2172.
RELECOMMUNICATION INFORMATION:
TELEFPAX: (202) 861-3000
TELEFAX: (202) 82-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 base pairs
                                                                                                        Db 14772 tttcccctcctgctttatct 14791
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Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) US-08-332-766A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 GGAGGGAGGGAAGGA 170
                                                                                    75 tttcccctcctgctttatct 94
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                     Best Local Similarity 100. Matches 20; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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US-08-332-766A-27
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    Query Match
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5.3%; Score 19; DB 2; Length 494;
100.0%; Pred. No. 1.7;
Live 0; Mismatches 0; Indels
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Patent No. 5850020
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Grierson, Alastair
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                            COUNTRY: U.S.A.

ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,000
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWAR:
FILING DATE: 21-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                      CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Speckman Picard PLLC
2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/332,766A FILING DATE: 01-NOV-1994
                                         1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELERX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-332-766A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 494 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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Matches 19; Conserva
                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2601 E
CITY: Seattle
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APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
WUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
                                                                                                                                                                             Sequence 9, Application US/09211710A

Sequence 9, Application US/09211710A

Sequence No. 6204434

GENERAL INFORMATION:

APPLICANT: Blocksberg, Leonard N.

APPLICANT: Havukkala, Ilkka

APPLICANT: Havukkala, Ilkka

APPLICANT: Grierson, Alastair

TITLE OF INVENTION: Matorials and Methods for the

FILE REPRENCE: 11000.1003c3

CURRENT APPLICATION NUMBER: US/09/211,710A

CURRENT APPLICATION NUMBER: US/09/211,710A

CURRENT FILING DATE: 1998-12-14

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 9

LENGTH: 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 624;
1.7;
          Indels
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APPLICATION NUMBER: US/08/975,316
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: September 11, 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 45, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%; Scor.
100.0%; Pre
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
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                                              169 gctgggcgtgctggctgag 187
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        19; Conservative
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: SLEATH, Janet REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pinus radiata
US-09-211-710-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
          Matches
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Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, IIkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                             Score 19; DB 2; Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 624;
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: EastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
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Mismatches
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                                                                  11000.1003
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APPLICATION NUMBER: 08/713,000
FILLIG DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                      REPERENCE/DOCKET NUMBER: 31,000;
REPERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0563
TELEPAX: 206-269-0563
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTER STILES:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
TOPOLOGY: linear
US-08-713-000-9
                                                                                                                                                                                                                                                                                                                           Query Match 5.3%; Sc
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.3%; 8
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                                                                                                                                                                                                                                                                                                                                                                                                         169 gctgggcgtgctggctgag 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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US-08-975-316-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-975-316-9
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                                                                                                                                                                                           Length 684;
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                                                                                                                                                                                                                                0; Indels
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Sequence 8, Application US/08705771

Sequence 8, Application US/08705771

GENERAL INC. 6054289;

APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu

TITLE OF INVENTION: Expression Products

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARLLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                           Query Match 5.3%; Score 19; DB 2; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 19; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCRNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELECHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.7;
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CLASSIFICATION: 536
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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100.0%; Pie
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1344 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 ggaggagggagggaa 344
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                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                  INFORMATION FOR SEQ ID NO:
TELEFAX: 206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-705-771-8
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                                                                                                                         linear
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US-08-975-316-45
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Sequence 13, Application US/08765662

Patent No. 5929213

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.0%; Score 18; DB 4; Length 2407; Best Local Similarity 100.0%; Pred. No. 5.5; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                               GREERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
FITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE PEFERRACE: BB-1199
CURRENT APPLICATION NUMBER: US/09/370,807
CURRENT FILING DATE: 1999-08-09
FARLIER APPLICATION NUMBER: 60/096,225
BARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 2407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,662
FILING DATE: 28-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
ATTING ADTE: 12-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A
REGISTRATION NUMBER: 38.347
REFERENCE/DOCKET NUMBER: 07265/0428
                         Sequence 7, Application US/09370807
Patent No. 6297034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 gctttgcagcaataactg 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Oryza sativa US-09-370-807-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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US-09-370-807-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: STATE:
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Sequence 1, Application US/09173914

Sequence 1, Application US/09173914

Sequence 1, Application US/09173914

Patent No. 6171857

GENERAL INFORMATION:

APPLICANT: Hendrickson, Eric

TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity

TITLE OF INVENTION: ANO. 6174857el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: A No. 617487el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: A No. 617487el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: A No. 61744 Methods of Regulating DNA Dependent Protein Kinase Activity

CURRENT APPLICATION NUMBER: 05/064,557

EARLIER PILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 6078
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Sequence 1, Application US/08483376;
Patent No. 595530
GENERAL INFORMATION:
APPLICANT: Vasil, vimla
APPLICANT: Clancy, Maureen A.
APPLICANT: Ferl, Robert J.
APPLICANT: Hannah, L. C.
TITLE OF INVENTION: No. 5955330el Means for Enhancing General Englishment of September 1 Transport of September 2 Transport of September 2 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of September 3 Transport of 
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                   0; Indels
                   Mismatches
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                                                                          330 gagggagggagggaagga 347
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                18; Conservative
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US-09-173-914-1
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ORGANISM: Homo Sapiens
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(2175).
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US-08-483-376-1/c
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NAME/KEY:
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                Matches
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GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                            5.0%; Score 18; DB 2; Length 2419;
100.0%; Pred. No. 5.5;
Live 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5099
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SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                       ; NAME/KEY: Coding Sequence; LOCATION: 218...1267
; COTHER INFORMATION:
US-08-765-662-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1563 GGAGGGAGGGAAGG 1580
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LOCATION: 218...1267

OTHER INCRMATION:

PCT-US95-08745-13
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Best Local Similarity 100.0
Matches 18; Conservative
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FRATURE:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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Best Local Similarity
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STATE: CA
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ORIGINAL SOURCE:
FEATURE:
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PCT-US95-08745-13
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us-09-846-456-2.oli.rni

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CURRENT READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/48,376
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US/08/418,540
FILING DATE: 07-APR-1995
PRIOR APPLICATION NUMBER: US/08/418,540
FILING DATE: 07-APR-1995
PRIOR APPLICATION NUMBER: US/08/410,115
APPLICATION NUMBER: US/08/410,115
APPLICATION NUMBER: US/08/30,956
FILING DATE: 04-AUG-1993
PRIOR APPLICATION NUMBER: US/07/830,956
FILING DATE: US-FEB-1992
PRIOR APPLICATION NUMBER: US/07/353,854
FILING DATE: 18*MAY-1989
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 10-94B
TELECOMMUNICATION NUMBER: 33,878
REFERENCE/COCKET NUMBER: US/08/08/09
INFORMATION FOR EQ. ID NO: 1:
SEQUENCE: CHARACTERISTICS:
LENGTH: 6386 base pairs
TELENGTH: 6386 base pairs
TELENGTH: 6386 base pairs
TTYPE: nucleic acid
STRANDEDSES: double
TOWNEY: Innear
ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201
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MOLECULE TYPE: DNA (genomic)
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2605..2728
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3447..3620
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2822..3038
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1828..1948
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3256..3351
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1211..1324
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2041..2187
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STRAIN: Black Sweet
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                                       Boulder
Colorado
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ORIGINAL SOURCE:
ORGANISM: Zea
                                                                           RY: US
80303
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
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FEATURE:
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ZIP: 4834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
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US-08-814-095-7/c
Sequence 7, Application US/08814095
Patent No. 6025183
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NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                          exon
4517..4835
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4768..5212
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5372..5510
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5636..5917
 exon
3702..3818
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                                                    3912..4078
                                                                                   exon
4158..4381
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NAME/KEY:
LOCATION:
                                        NAME/KEY:
LOCATION:
                                                                                NAME/KEY:
LOCATION:
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FEATURE:
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US-08-483-376-1
                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                       LOCATION:
                                                                                                        FEATURE:
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TOPOLOGY: linear

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CDENTIFICATION WETHOD: experimental

OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: /4110)"

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /gene= "ACHE"

OTHER INFORMATION: /gene= "ACHE"
                                                                                                                                                                                                                                 NAME/KEY: promoter LOCATION: 4089..22464 OTHER INFORMATION: /function= "ACHE Promotor" OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenite resistance
OTHER INFORMATION: gene"
OTHER INFORMATION: /gene= "AR"
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 22465..22537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 3
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IDENTIFICATION METHOD: experimental
OCHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE" OTHER INFORMATION: /number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: complement (34092..34358)
                                                                                                                                                                                          CHROMOSOME/SEGMENT: 7q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 24090..25177
                                                                                                                                           ORGANISM: Homo sapiens
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 22465..22537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: terminator
LOCATION: 27385..27387
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LOCATION: 28129..28131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                    HYPOTHETICAL:
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NAME/KEY: exon
LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 8
FEATURE:
NAME/KEY: exon
LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene="AR"
                                                                                                                                                               NAME/KEY: exon
LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
                                                               NAME/KEY: exon
LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
                                                                                                                                                                                                                                                                                                                LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
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LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 13
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
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: LOCATION: complement (29664..29856)
: OTHER INFORMATION: /gene="ARS"
US-08-814-095-7
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
                                                                                                                                                                                                                                                                                         NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon LOCATION: compl
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NAME/KEY: exon
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NAME/KEY: exon
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LOCATION: compl
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APPLICANT: HENGLEIN, Berthold
APPLICANT: ZINDY, Fr d rique
TITLE OF INVENTION: NEW HUMAN CYCLIN A COMPOSITIONS AND A
TITLE OF INVENTION: PROCESS FOR THEIR PRODUCTION, THE CORRESPONDING NUCLEOTIDE
TITLE OF INVENTION: A PROCESS AND AGENTS FOR CELL PROLIFERATION DETECTION OR DI
TITLE OF INVENTION: AND A PROCESS AND AGENTS FOR INHIBITING CELL PROLIFERATION.
NUMBER OF SEQUENCES: 1
      APPLICANT: HENGLEIN, Berthold
APPLICANT: ZINDY, Er d rique
TITLE OF INVENTION: NEW HUMAN CYCLIN A COMPOSITIONS AND A PROCESS FOR THEIR PRO
NUMBER OF SEQUENCES: 1
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100.0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cyclin A coding sequence from base 97 to base 1392, coding for a protein of 432 amino acids.
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette-5.25 inch, 500 Kb storage
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC/XT/AT or compatibles
OPERATION SYSTEM: MS-DOS VERSION 3.0 or above
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,895
FILING DATE: O5-UNN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Larson and Taylor
STREET: 727 Twenty-Third Street, South
                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Larson and Taylor
STREET: 727 Twenty-Third Street, South
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/650, 805
FILING DATE: 06-FEB-1991
APPLICATION NUMBER: FR9001596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FR9001596
FILING DATE: 12-FEB-1990
INFORMATION FOR SEQ ID NO: 1 :
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09210889; Patent No. 6103887; GENERAL INFORMATION: APPLICANT: BRECHOT, Christian APPLICANT: CHENIVESSE, Xavier
CHENIVESSE, Xavier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 1165 CAGCAATAACTGATGGC 1149
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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ZIP: 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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COCATION:
US-08-460-895-1
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APPLICANT:
                                                                                                                                                                                                                 COUNTRY:
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STATE:
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                                           5.0%; Score 18; DB 3; Length 35060; 100.0%; Pred. No. 5.7; tive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION TO 435
PRIOR APPLICATION NUMBER: 08 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, DONALD J.
REGISTRATION NUMBER: 25,323
                                                                                                                                                                                                                                                              Sequence 4, Application US/08332766A
; Sequence 4, Application US/08332766A
; Patent No. 2843647;
; GERERAL INFORMATION:
    APPLICANT: JEFFREYS, Alec J.
    APPLICANT: ARMOUR, John
    TITLE OF INVENTION: SIMPLE TANDEM REPEATS
    NUMBER OF SEQUENCES: 125
    CORRESPONDENCE ADDRESS:
    ADDRESSE: CUSHMAN DARBY & CUSHMAN, L.L.P.
    STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%; Score 17; DB 2;
100.0%; Pred. No. 17;
tive 0; Mismatches
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US-08-460-895-1/c
US-08-460-895-1/c
Sequence 1, Application US/08460895
Patent No. 5849508
GENERAL INFORMATION:
APPLICANT: BRECHOT, Christian
APPLICANT: WANG, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                 Db 23954 GAGGGAGGGAGGGAAGGA 23937
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TELEFAX: (202) 822-0944
TELEEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
                                                                                                                                      330 gagggagggagggagga 347
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                                                    Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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Best Local Similarity
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RY: U.S.A.
20005-3918
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COUNTRY: USA
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US-09-097-199-8
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4.8%; Score 17; DB 3; Length 1634;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels
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Patent No. 5882864
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: Ralph, David
APPLICANT: Ralph, David
APPLICANT: Nobert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE
NUMBER OF SEQUENCES: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cyclin A coding sequence from base 97 to base 1392, coding for a protein of 432 amino acids.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 500 Kb storage COMPUTER: IBM PC/XT/AT or compatibles OPERATING SYSTEM: MS-DOS version 3.0 or above SOFTWARE: WORD PERPECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/08/692,787
FILING DATE: Concurrently Herewith
APPLICATION: 514
                                                                                                                                                                             PULICATION DATA:
APPLICATION NUMBER: 07/650, 805
FILING DATE: 06-FEB-1991
APPLICATION NUMBER: FR9001596
FILING DATE: 12-FEB-1990
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: nucleic acid
SYRANDEDNONES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Corder, Timothy S. REGISTRATION NUMBER: 38,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1165 CAGCAATAACTGATGGC 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS
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ADDRESSEE: Arnold, W
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                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Texas
                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-692-787-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-210-889-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
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                                                                                                                                                                                                                                                   Ouery Match
4.8%; Score 17; DB 2; Length 1649;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: NAKASINIMA, RICHARDA
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: URCC:018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09097199
Patent No. 6218529
TELEPHONE: (512) 418-3000
TELEBRAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                 56 cagcaataactgatggc 72
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US-08-692-787-8
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Best Local Similarity
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Sequence 0. 6277981

GENERAL INFORMATION:
APPLICANT: Tu, Guang-Chou
TITLE OF INVENTION: A NITSENSE OLIGONUCLECTION OF
TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLECTIDES
FILE REFERENCE: 9855-301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.8%; Score 17; DB 4; Length 80246; 100.0%; Pred. No. 19; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09078294
Patent No. 6265211
GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION UNMER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOUTHARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 80595
                                                                                                   APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A MOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER: OF SEQ. ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA; ORGANISM: Nucleotide sequence of NC-contig
US-09-078-294-4
                                     ; Sequence 4, Application US/09078294
; Patent No. 6265211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 21743 GGAGGGAGGGAGG 21727
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 44
US-09-078-294-3/c
                                                                                                                                                                                                                                                                                                                                     LENGTH: 80246
RESULT 43
US-09-078-294-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-109-663-14
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CURRENT APPLICATION NUMBER: US/09/109,663

CURRENT FILING DATE: 1998-07-03

EARLIER PEPLICATION NUMBER: 60/051,705

EARLIER PEPLICATION NUMBER: 60/051,705

EARLIER FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 81

SEQ ID NO 14

LENGTH: 21

TYPE: DNA

OTHER INFORMATION: Description of Artificial Sequence: Candidate

COTHER INFORMATION: TRF(alpha) ASO

OTHER INFORMATION: TRF(alpha) ASO

US-09-109-663-14

Query Match

Best Local Similarity 100.0%; Pred. No. 51;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 334 gagggaggaaggaag 349

[|||||||||||||||||||||||

Db 3 gagggagggaaggaag 18

Search completed: September 20, 2002, 06:15:23

Job time: 11142 sec
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 04:07:18; Search time 3900.56 Seconds

(without alignments)
1235.313 Million cell updates/sec
Perfect score: 357
Sequence: 1 tggaggtctcagctgagagg......gagggaaggaagctgtgtg 357
Scoring table: 0LIGO_NUC
Gapop 60.0, Gapext 60.0
Searched: 13736207 seqs, 6748477542 residues

Word size: 0
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: em\_estba:\*
2: em\_esthum:\*
3: em\_esthum:\*
4: em\_estin:\*
5: em\_estov:\*
6: em\_estov:\*
6: em\_estov:\*
7: em\_estor:\*
11: gb\_esti:\*
11: gb\_htc:\*
12: gb\_gss:\*
13: em\_gss\_inv:\*
14: em\_gss\_lnv:\*
15: em\_gss\_lnv:\*
16: em\_gss\_vrt:\*
16: em\_gss\_vrt:\*

Post-processing: Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	\$ Query Match	% Query Match Length DB	DB	OI.	Description
	51	14.3	736	. 6	AU135588	AU135588 AU135588
7	39	10.9	535	10	BG384217	BG384217 303216 MA
e	24	6.7	158	12	AQ508395	AQ508395 RPCI-11-2
4	24	6.7	292	10	244377	Z44377 HSC1ZB081 n
υ 2	24	6.7	709	12	AQ528018	AQ528018 RPCI-11-3
0	24	6.7	716	12	AG163359	AG163359 Pan trogl
7	23	6.4	401	6	AI394181	AI394181 tq67a04.x
ω υ	23	6.4	827	12	B20638	B20638 F15016-T7 I
0	22	6.2	282	σ	BE050974	BE050974 za71c12.g
10	22	6.2	309	12	BH293527	BH293527 CH230-30L
c 11	22	6.2	371	10	BF592428	BF592428 7156a03.x
12	22	6.2	406	10	R11136	R11136 yf39b09.rl
c 13	22	6.2	465	σ	AI481405	AI481405 vg17d11.x
c 14	22	6.2	478	σ	BE050973	BE050973 za71c12.b
c 15	22	6.2	483	12	AZ654841	AZ654841 1M0529P18
c 16	22	6.2	515	12	BH337839	BH337839 CH230-194
c 17	22	6.2	523	10	BM310687	BM310687 iq47b12.y

AZ647100 1M0513122 AQ415718 RPCI-11-2 AQ938157 AQ078910 CIT-HSP-2 AZ078099 1M01226P8 AZ828464 ZM0105N23 AQ924975 RPCI-23-2 B70930 CIT-HSP-206 BF984535 G02307723 AZ74261 RPCI-23-2 BF077424 60146462 BF6817824 6014641977 BF617281 601441977 BF617281 601434197 AZ951107 RPCI-24-1 AZ095117 RPCI-24-1 AZ095117 RPCI-24-1 AZ055509 1M0562002 F11105 HSC2TE032 N AZ55509 1M0360B02 BS0482 CIT-HSP-437	mRNA linear EST 24-OC clone PLACE1002437 5', mRNA niata; Vertebrata; Euteleost arrhini; Hominidae; Homo.	nayY., Nagal,T., Sugano,S.  0812, Japan  end one pass sequencing: construction: Department ience, University of Toky  " 0 t 5 others
AZ647100 AQ185718 AQ38157 AQ078910 AZ078910 AZ078910 AZ078464 AQ88455 BF617424 BF617424 BF617424 BF617424 BF617424 BF617424 BF617424 BF617424 BF617424 BF61743191 AZ51915 AZ51915 AZ51056 AZ11105 AZ656509 F1105 AZ656509 F1105 AZ656309 F1105 AZ656309 F1105 AZ656309	Σ Ωυ >	Naka niba 29 5' - & 3 5' - & 3 iers sapien :9606" 20406" TEI" lacenta
	Homo .09961 .093 ( .0a; (	kamatsu, kamatsu, 00) Isogai tory Insriu 3951 3951 3951 3951 00 00 00 00 00 00 00 00 00 00 00 00 00
522 5245 5269 5273 5273 5273 6215 6215 6216 6216 6216 6216 6216 6216	GI:1 GI:1	J., Wakamatsu,A J., Wakamatsu,A CDNA project ed (2000) Takao Isogai Laboratory each Institute na, Kisarazu, Cl 38-52-3951 38-52-3951 nomics@hri.co.jl CDNA project; Institute of NA Institute of NA Institute of NA Institute ichna Cocation/Qualif. J. 736 Ad_Leref="Laxon/Ad_Leref="Homo/Ad_Leref
, , , , , , , , , , , , , , , , , , ,	AU135588 PLA AU13588 PLA AU13588 AU135588 AU135588.1 EST. human. human. humo sapiens Eukaryota Eukaryota mammalia; Eu	Vota'.', Albana Isogai,T.' Wamannoto,J.' W Isogai,T.' Wanbubbed (20 Contact: Takao Genomics Labor Helix Research 1532-3 Yana, K Tel: 81-438-52 Fax: 81
	AU135 AU135 AU135 AU135 AU135 AU135 EST. Homen Homen	Vota 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AU131588 LOCUS DEFINITION ACCESSION VERSION VERYWORDS SOURCE ORGANISM	Č.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 158)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Conservative
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                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Best Local Similarity
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               ORGANISM
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COMMENT
                                                                REFERENCE
                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
Z44377
SOURCE
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, DNA sequence.
AQ508395.1 GI:4713142
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred vo. 980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS
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                                                                                                                                                                                            EST 12-MAR-2001
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                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 535)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                    Design and use of two pooled tissue normalized cDNA libraries for Ext discovery in swine Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Llbrary made from pooled tissue from day 11, 13, 15, 20, and 30 amhrunc "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                               Gaps
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                                                                        Length 535;
               Length 736;
                                                                                                                                                                        535 bp mRNA linear 303216 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BG384217.1 GI:13308689 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
           14.3%; Score 51; DB 9; Le
100.0%; Pred. No. 1.8e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 ctgctgtggaagaacctcactttcagaagaagacaaaca 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 39; DB illarity 100.0%; Pred. No. 1.6 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: G column: 13
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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                                           51; Conservative
                            Best Local Similarity
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Best Local Similarity
Matches 39; Conserv
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Sus scrofa
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                                          Matches
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HSC1ZB081 normalized infant brain cDNA Homo sapiens CDNA clone 2.12b08, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong Pieter-Rédorng med. buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: SP6 class: BAC ends.
Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Eorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                    Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 24; DB 12; Length 158;
100.0%; Pred. No. 0.37;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Unpublished (1997)
Other GSSs: RPCI-11-274EIL.TV
Other GSSs: RPCI-11-274EIL.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
771: 301 838 0208
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="RPCI-11-274E11"
/clone_lib="RPCI-11"
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1. .158
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source

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/tissue_type="total brain"
/dev.stage="3 months old"
/dev.stage="3 months old"
/note="Corgan: brain, Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev.stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(df) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press" 3 others
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Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library availability, please contact Pieter de Jong

(pieter@deejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
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                                            Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lzb08
Seq primer: (-21)M13_universal.
Location/Qualifiers
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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100.0%; Pred. No. 0.4;
tive 0; Mismatches 0; Indels
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Other GSSs: RPCI-11-313F19_TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-1zb08"
/clone_lib="normalized infant brain cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AGCTCTGGCCGCTGCCTTCCAGGG 259
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                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
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Best Local Similarity 100.(
Matches 24; Conservative
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Fax: 301 838 0208
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Location/Qualifiers

FEATURES

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Lotass, A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Direct Submission
Direct Submission
Ochanical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, WE:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax.81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCL-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end was generated during the R&D process and may have higher chance of clone tracking errors.
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AGI63359.1 GI:16693037
GSS; GSS (genome survey sequence).
GSS in troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-030B04.T7.
Pan troglodytes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                       /cer="______/ser=" /ser=" /ser=" /ser=" /ser=" /ser=" /ser=" /cell_type=" Lymphocytes" /ser="                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes DNA, clone: RP43-030B04.T7, genomic survey
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
246 c 84 g 268 t l others
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BAC end sequences of Library RPCI-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7%; Score 24; DB 12; Length 709;
100.0%; Pred. No. 0.44;
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/db_xref="taxon:9598"
/clone="RP43-030B04.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. .v.
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/db_xref="GDB:7619946"
/db_xref="taxon:9606"
/clone="RPOT-11:313F19"
/clone_lib="RPOT-11"
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 GGAGGGAGGGAGGGAAGGAAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
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Matches 24; Conservative
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Best Local Similarity
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Class: BAC ends
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/db_xref="taxon:9606"
/clone="Ixace:113806"
/clone="Ixace:13806"
/clone="Ixace="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="PulloB"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-34549, and 484488-489479."
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F15016-T7 IGF Arabidopsis thaliana genomic clone F15016, DNA
sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 480 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
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282 bp mRNA linear EST 08-JUN-2000 2a71c12.g51 Maize Glume cDNAs Library Zea mays cDNA clone za71c12 BE050974 EBE050974.1 GI:8368029 EST.
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(Shaughnessy,A.L., Habermann,K., de la Bastide,M., Huang,E.N.,
Nascimento,L.U., Schutz,K., Matero,A., Swaby,I., See,L.-H., Preston
A.R.R., Rodriguez,M.A., Shah,R.S., Shekher,M., Spiegel,L.A., Vil
M.D., Dedhia,N.N. and McCombie,W.R.
Expressed sequence tags from Zea mays (maize)
Unpublished (2000)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fex., 516 367 8884
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida; eurosida; II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 827)
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
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                                                                                                                                                                                                                                                                                                                                            Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
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100.0%; Pred. No. 1.4;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jecker@atgenome.bio.upenn.edu
Seq primer: T7
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233 c 90 g 284 t
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Arabidopsis Thaliana Genome Center
University of Pennsylvania
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High quality sequence stop: 226.
Location/Qualifiers
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Plate: za71 row: c column: 12
Seq primer: -40M13RevUniv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Columbia
                                                                                                                                                                         BAC End Sequences at ATGC
Unpublished (1997)
Other_GSSs: F15016-Sp6
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Fax: 215-898-8780
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact pieter de Jong (pdejongémail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 30 row: L column: 8
Seq primer: T7
Class: BAC ends.
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Jong,P. and Fraser,C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment (npublished (1999) other GSSs: CH230-30L8.TJ

Contact: Shaying Lab.

Contact: Shaying Lab.

Contact: Shaying Lab.

The Institute for Genomic Research
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/note="Vector: pTaRBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA linear GSS 30-NOV-200
CH230-30L8.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-30L8, DNA sequence.
                                   1. .282
/organism="Zea mays"
/d_xref="taxon:4577"
/db_xref="taxon:4577"
/clone="iaa712"
/clone_lib="Maize Glume cDNAS Library"
/note="Vector: Lambda Zap II (Stratagene); Site_1: XhoI; Site_2: EcoRI; Resistance: Ampicillin Autoexcision: pBluescript SK (+/-) Titer: 7 x 10e-9 pfu/mL (as of 9/28/94)"
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                 48 t
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-30L8"
                                                                                                                                                                                                                                                                                              6.2%; Score 22; 100.0%; Pred. No.
High quality sequence stop: 282,
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36 c 8
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Best Local Similarity 100.u
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissaue Procurement: Dennis Stori, M.D., Kristina Cole, M.D., Ph.D.

student, Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: breast; Vector: pAMP1; mRNA made from breast carcinoma tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 400 bp. Primary library, non-amplified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS R11136 406 bp mRNA linear EST 11-APR-1995
DEFINITION yf39b09.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                        7156a03.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338668 3' similar to contains element TAR1 TAR1 repetitive element ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 371)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov from Gibco.
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  DB 12; Length 309; 3.9;
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/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_Br16"
/sex="female"
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Ouery Match 6.2%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 3.9 Matches 22; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Processive 0;
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                                                                                                             328 aggagggagggaggaag 349
                                                                                                                                                                278 AGGAGGGAGGGAAGGAAG 299
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100.0%; Pred. No. 4.1;
tive 0; Mismatches
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/db_xref="taxon:10090"
/clone="IMAGE:861621"
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Matches 22; Conservative
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/db_xref="GDB.481370"
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/db_xref="GDB.481370"
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/dev_stage="20 week-post conception fetus"
/dev_stage="10 week-post conception fetus"
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/dev_stage="10 week-post conception fetus"
/dev_stage="20 week-post conception fetus"
/dev_stage="10 week-post conception fetus"
/dev_stage="10 week-post confided profiled p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
Insert Size: 2665
High quality sequence stops: 290 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2665 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 290.
                                                                                                                                                                                                                                                                                   (bases 1 to 406)

Hillar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston Tre, Washu-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 bp mRNA linear EST 09-MAR-1999 9917dl1.x1 Soares mouse NbMH Mus musculus cbNA clone IMAGE:861621 3', mRNA sequence.
IMAGE:129209 5' similar to qb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN ):contains MER22 repetitive element ;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (bases 1 to 478)
O'Shaughnessy,A.L., Habermann,K., de la Bastide,M., Huang,E.N.,
Nascimento,L.U., Schutz,K., Matero,A., Swaby,I., See,L.-H., Preston
Y.R.R., Rodriguez,M.A., Shah,R.S., Shekher,M., Spiegel,L.A., Vil
M.D., Dedhia,N.N. and McCombie,W.R.
Expressed sequence tags from Zea mays (maize)
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1 (bases 1 to 465)
Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 18
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                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
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/sex="male"
/tissue_type="heart"
/dev_stage="4_weeks"
/lab_host="DH108"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0529P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 483)
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                                                                                                                                                                                                                                                                                                                        /clone_lib="Maize Glume cDNAs Library"
/note="Wector: Lambda Zap II (Stratagene); Site_l: XhoI;
Site_2: BcoRI: Resistance: Ampicillin Autoexcision:
pBluescript SK (+/-) Titer: 7 x 10e-9 pfu/mL (as of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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  Unpublished (2000)
Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
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Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: P column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone UUGC1M0529P18 F, DNA sequence.
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/strain="C57BL/6J"
                                                                                                                                        Email: mccombie@cshl.org
Plate: za71 row: c column: 12
Seq primer: -40Ml3ForUniv
High quality sequence stop: 478.
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Location/Qualifiers
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/clone="UUGC1M0529F18"
                                                                                                                                                                                                                                                               /organism="Zea mays"
/db_xref="taxon:4577"
/clone="za71c12"
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170 c 127 g
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Fax: 801 585 7177
                                                                                                                                                                                                                                          .478
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with THA DNA polymerase and THA polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwwl. (1972.114) [ab] API.29072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Lao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de And Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)

Other_GSSs: CH280-19479.TJ

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 194 row: J column: 9
Seq primer: T7
Class: BAC ends.
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CH230-194J9, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                            Laboratory Mouse DNA Resource
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/sex="Male"
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                                                                                                                         Query Match
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Not!; Site_2: Xho!; CDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size-1kb. 5'
Xho! Site was destroyed after directional clouhing.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Buchid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dass 1 to 523)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Hellshaka, T., Scaerce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, J., and Bowers, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Williams, T. Endocrine Pancreas Consortium
               /strain="BN/SSRHSd/MGW"
/db_xref="taxon:10116"
/db_xref="taxon:10140"
/clone_lib="cH20-19409"
/sex="Female"
/sex="Female"
/note="tayon"
/note="tayon:"pranhsd/McW) BAC library produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
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Endocrine Pancreas Consortium
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BM310687
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                                                                                                                                                                                                                                                                                                                                    Query Match 6.2%; Score 22; DB 12; Length 515; Best Local Similarity 100.0%; Pred. No. 4.2; Matches 22; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/db_tofone_lib="HRRS islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/organism="Rattus norvegicus"
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Other_ESTs: ig47b12.x1
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473214 gbplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="UUGC1M0513L22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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314-362-1916, Fax: 314-747-2692."
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Insert Length: 10000 Std Error:
Plate: 0513 row: L column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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RPCI-11-204G24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-204G24
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 156\ c 91 g 183\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
thtp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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                                                                                                   DB 12; Length 525; 4.2;
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Other GSSs: RPCI-11-204G24.TJ
Other GSSs: RPCI-11-204G24.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                                                                                                                     0; Indels
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/db_xref="GDB:7578119"
/db_xref="taxon:9606"
/clone="RPCI-11-204G24"
/clone_lib="RPCI-11"
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AQ415718
AQ415718.1 GI:4474687
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Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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CIT-HSP-2367J11.TR CIT-HSP Homo sapiens genomic clone 2367J11, DNA
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/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
a 175 c 1129 t
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(Dases 1 to 569)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSS: CIT-HSP-2367J11.TF
AV938157 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum AV938157
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1 (bases 1 to 552)
Sato,K., Saisho,D. and Takeda,K.

Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hordeum vulgare subsp. spontaneum"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 311 838 0200
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Best Local Similarity 100.0%; Pred. No. 4.2
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Location/Qualifiers
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                                                                 Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3 Reverse
Class: BAC ends.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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100.0%; Pred. No. 4.2;
Live 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0132 row: P column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/clone="2367J11"
/clone_lib="CIT-HSP"
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                           Email: mdadams@tigr.org
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Fax: 301 838 0208
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(http://www.jax.orgyrescources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qilq732114[qb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
RR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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2M0105N23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
/clone="UUGC2M0105N23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Wale"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Fax: 801 585 7177
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                                                             (http://www.fax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and T4 polymerase active states. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) pblAR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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RPCI-23-277Ell.TV RPCI-23 Mus musculus genomic clone RPCI-23-277Ell
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
Plate: 277 row: E column: 11
Seq primer: 77
Class: BAC ends.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 615)
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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100.0%; Pred. No. 4.2;
tive 0; Mismatches 0; Indels
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Contact: Shaying Zhao Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fel: 301 838 0200
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/db_xref="taxon:10090"
/clone="RPCI-23-277E11"
/clone_lib="RPCI-23"
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Matches 22; Conserv
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/sex="Female"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Grgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 623)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.iigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mi3.21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a random BAC End Sequence Database for Sequence-Ready Map Building
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                  6.2%; Score 22; DB 12; Length 615; 100.0%; Pred. No. 4.2; tive 0; Mismatches 0; Indels
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other GSSS: CIT-HSP-2063G10.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:7061533"
/db_xref="taxon:9606"
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/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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AQ983682

754 bp DNA linear GSS 30-JAN-2000

RPCI-23-323J22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-323J22

, DNA sequence.

AQ983682
                                                                                                                                                                                                                                                                                                                                   Email: szhao@typr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 74 row: G column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male" //cell_type="Spleen/Brain" //cell_type="Spleen/Brain" //note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Wouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using Mbol partially digested male C57BL/6J
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 754)
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Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pleter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 22; DB 12; Length 713;
                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Contact: Shaying Jay Contact: Shaying Jay Shaying Jay Shaying Jay Shaying Jay Shaying Jay Shaying Jay Shajing Shajing Shajing Shajing Shajing Shaj
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   Russell, D., de Jong, P. and Fraser, C.M. Mouse BAC End Sequences from Library RPCI-24 (Unpublished (1999) Other_GSSS: RPCI-24-74G13.TV
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                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
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/clone="RPCI-24-74G13"
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                                                                                                                                            Contact: Shaying Zhao
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AQ983682/c
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                                   TITLE
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KEYWORDS
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                                                                                                     COMMENT
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/db_xref="taxon:9606"
/dbox="InAdE:439906"
/clone=lib="InAdE:439906"
/clone=lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_host="hulb@ (phage-reasistant)
/tab_host="nilb@ (phage-reasistant)
/note="Organ: small intestine; Vector: pCWV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                        BF984535 673 bp mRNA linear EST 23-JAN-2001 602307723F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4399276 5',
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RPCI-24-74G13.TJ RPCI-24 Mus musculus genomic clone RPCI-24-74G13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E 1 (bases 1 to 673)

S NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Arroy

Tissue Procurement: Arroy

Tissue Procurement: Arroy

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequenching by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

plate: LLAMN10102 row: m column: 05
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 713)
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
                               491 AGGAGGGAGGGAGGGAAGGAAG 470
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Best Local Similarity 100.0%; Pr
م، ممهودی
328 aggagggagggaggaag 349
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A2742461
A2742461.1 GI:12521331
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                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C5/BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially diagested
with a combination of EcoRI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies).

a 189 c 131 g 251 t lothers
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/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/tabost="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 323 row. J column: 22 Seg primer: SP6 Class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can be
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+ive 0; Mismatches
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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Plate: LLAM9667 row: k column: 15
High quality sequence stop: 678.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                         /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="RPCI-23-323J22"
/clone_lib="RPCI-23"
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Matches 22; Conserv
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926 bp mRNA linear EST 22-MAY-2001
602728977F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4868443 5',
mRNA sequence.
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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Olone="13846235"
/Clone="11b="NIH_MGC_65"
/Lissue_type="adenocarcinoma"
/Lissue_type="adenocarcinoma"
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
#Notarge insert size 1.8 kb. Library constructed by Life
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  Library constructed by Life
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMSSE row: i column: 20
High quality sequence start: 8
High quality sequence stop: 660.
Location/Qualifiers
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100.0%; Pred. No. 4.4;
cive 0; Mismatches 0; Indels
                                                                                                                     Score 22; DB 10; Length 760;
Pred. No. 4.3;
                                                                                                                                                               0; Indels
Average insert size 1.1 kb.
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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BE617281.1 GI:9888219
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Clone distribution: MGC clone distribution information can be
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Plate: 0.280 row: 0 column: 18
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Homo sapiens"
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                                                                                                                                                                       /db_xref="taxon:9606"
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/clone_lib="NIH_MGC_15"
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/clone="UUGC2M0280018"
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                                                                                                               Location/Qualifiers
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Fax: 801 585 7177
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Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dlone=Trange:486443"
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/clone=lib="NIH_MGC_15"
/tlssue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into BcoRI/XhoI sites using the following 5' adaptor: GGCACGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
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NIH-NGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1738 row: i column: 20
High quality sequence stop: 728.
Location/Qualifiers
                                                                                                                                                                MINIMOC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Pragatation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
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Best Local Similarity 100.0%; Pred. NO. ....
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                      BG823588.1 GI:14171175
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                                                                                    Homo sapiens
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plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Aslam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Pred. No. 4.5;
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1233 row: f column: 24
High quality sequence stop: 668.
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/clone="UUGC1M0090K10"

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source
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                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase 
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Mus musculus

Mus area (Cordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 51)

1 (bases 1 to 51)

Morgan, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                           /lab_host="E. coli strain XL10-Gold, T1-resistant, F-" /note="Weetor: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ351915 51 bp DNA linear GSS 29-SEP-20G MO099K10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0090K10 F, DNA sequence.
AZ351915
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 51.
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∕organism÷"Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
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                                              /sex="Female"
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Matches 21; Conservative
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Fax: 801 585 7177
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/Grown-Libe Woulde LUKD pissing occurs included.
//sex "Wale"
//lab_host="E. Coli strain XLIO-Gold, TI-resistant, F-"
//note="Vector: PWD42DY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated bassage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by respected for sheared
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1M0338H04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0338H04 R, DNA sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah

Rm. 138, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/clone_lib="Mouse 10kb plasmid UUGClM library"
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Fax: 801 585 7177
Email: ddunndgenetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0338 row: H column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
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AZ500262.1 GI:10679897
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ORGANISM
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AZ838528/c
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                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gplAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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IM0185006F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Weetcr: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
/db_xref="taxon:10090"
/clone="UUGCIM0338H04"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 5.9%; Score 21; DB 12; Length 62; Best Local Similarity 100.0%; Pred. No. 10; Matches 21; Conservative 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error:
Plate: 0185 row: o colunn: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLL0-Gold (Stratagene) cells and selected for ampicialin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Lislam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 90.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                            /db_xref="taxon:10090"
/clone="UUGC1M0185006"
/strain="C57BL/6J"
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                                                                                                                                        /sex="Male"
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qbb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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RPCI-24-146C22.TJ RPCI-24 Mus musculus genomic clone RPCI-24-146C22
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
age: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 146 row: C column: 22
Seq primer: SP6
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J. (bases 1 to 120)
Jaho, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Ungublished (1999)
Other GSSS: RPCI-24-146C22.TV
                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Vector: PWA2nv; Purified genomic DNA from M. musculus C57BL/57 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/organism="Mus musculus"
                    /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0134E17"
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                                                                                                                                      /sex="Male'
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissaue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael
Tissaue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael
R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd.ET from Amersham.
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qi70c08.xl NCI_CGAP_Ov26 Homo sapiens cDNA clone IMAGE:1861838 3'
similar to contains element TAR1 TAR1 repetitive element ;, mRNA
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                                                                                                                                                                            /cell_type="Spleen/Brain"
/note="Vector: pTARBAG1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAG1 cloning vector at the
BamH1 sites using MboI partially digested male CS7BL/6J
DNA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 145)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Taxional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Pred. No. 11;
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100.0%; Pred: No. 11.
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/db_xref="taxon:9606"
/clone="IMAGE:1861838"
/clone_lib="NCI_CGAP_Ov26"
                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-146C22"
/clone_lib="RPCI-24"
/sex="Male"
                                             /organism="Mus musculus"
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Location/Qualifiers
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
                                                                               Gaps
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100.0%; Pred. No. 12;
tive 0; Mismatches 0; Indels
Query Match 5.9%; Score 21; DB 9; Length 145; Best Local Similarity 100.0%; Pred. No. 11; Matches 21; Conservative 0; Mismatches 0; Indels
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Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="taxon:10090"
/clone="RPCI-23-7H17"
/clone_lib="RPCI-23"
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Best Local Similarity 100.0
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwbAc2 (gil47321141gbAr129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
A2457379 191 bp DNA linear GSS 04-OCT-2000 IMO260L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0260L10 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191)
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//ab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGCIM0260L10"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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100.0%; Pred. No. 12;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0260 row: L column: 10
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Class: plasmid ends
High quality sequence stop: 191.
Location/Qualifiers
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Best Local Similarity 100.0
Matches 21; Conservative
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Fax: 801 585 7177
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us-09-846-456-2.oli.rst

169 GAGGAGGGAGGGAGGA 189

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39 GGAGGGAGGGAGGAAGGAAG 19
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                                                                                                                A2656509 212 bp DNA linear GSS 14-DEC-2000 1M0532002F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0532002 F, DNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/strain="c57BL/6J"
/db_xref="taxon:10090"
/db_aref="taxon:20000"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 212)
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Fax: 801 585 7177
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/tissue_lige="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="corgan: brain, Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain;
cotal muRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, N.A.S in press" 3 others
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F11105 269 bp mRNA linear EST 12-MAR-1995 HSC2TE032 normalized infant brain cDNA Homo sapiens cDNA clone c-2te03 3', mRNA sequence.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 209)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Sebastiani Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genexpress@genethon.fr
Single read. 19T removed at sequence 5'end
Genexpress_lbrary_idt. C; Genexpress_sequence_idt: a3c-2te03
Seq primer: (-21)M13_universal.
Location/Qualifiers
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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/db_xref="taxon:9606"
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                                                                                                                         F11105.1 GI:705457
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                                                                                                                                                                                                                   Homo sapiens
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KEYWORDS
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Gaps ; 0

0; Indels

5.9%; Score 21; DB 12; Length 212;

100.0%; Pred. No. 12; tive 0; Mismatches

Best Local Similarity 100. Matches 21; Conservative

Query Match

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//ab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polywucleotide Kinase. Adaptor oilgonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
Contractity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B50482
CIT-HSP-437M12.TP CIT-HSP Homo sapiens genomic clone 437M12, DNA sequence.
B50482.1 GI:2602719
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 294)
                                                                                                                              Dunn, D., Agyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCIM0360B02"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: B column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
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High quality sequence stop: 294.
Location/Qualifiers
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Fax: 801 585 7177
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                              Mus musculus
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                       Kim,U.-J., Adams,M.D. and Simon,M.I.Determination of clone end sequences of human Bacterial Artificial
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 319)
                                                                                                                                                                                                                                                                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: SP6
Class: BAC ends.
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/note="Vector: pB@loBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                           Other_GSSS: CIT-HSP-437M12.TV
Contact: Ung-Jin Kim
CalTech Genome Research Lab
california Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA 91125, USA
Tel: 626 796 7066
Fax: 626 395 4901
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Job time: 13778 sec
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Enwer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abc1 gene
Patent: WO 0183746-A 4 08-NOV-2001;
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Sequence 4 from Patent WO0183746.
AX351032
AX351032.1 GI:18616388
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62 c 73 g 4.
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AX351029
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880.830 Million cell updates/sec
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                                                         September 20, 2002, 06:30:00; Search time 5250.46 Seconds
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                 1797656 seqs, 10463268293 residues
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                                            - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Ar.258627 697 bp mRNA linear PRI 11-MAY-2000 Homo sapiens ATP binding cassette transporter 1 (ABCA1) mRNA, partial cds.
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SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKS"
198 c 190 g 156 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-APR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 9414-0130, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hARGI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

Biochem. Biophys. Res. Commun. 271 (2000) In press 2 (bases 1 to 697)

2 (bases 1 to 697)

Pullinger, C.R., Fielding, C.J. and Kane, J.P., Rug, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
                                                                                                                                                      61 ccgggctgcggcagggcagggcgggagctccgcgcaccaacagagccggttctcagggc 120
                                                                                                                                                                              61 CCGGGCTGCGGCAGGCAGGCAGGGAGCTCCGCGCACAACAAGCCGGTTCTCAGGGC 120
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/protein_id="AAF69513.1"
/db_xref="G1:7769708"
            Length 221;
                                              Indels
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100.0%; Pred. No. 5.1e-118;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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Length 697;

Score 221; DB 9; Pred. No. 5.2e-118;

100.0%; 100.0%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                           PRI 10-APR-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1167)
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Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for
Clinical Chemistry, University of Regensburg,
FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
Location/Qualifiers
                                                                83 GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTC 142
                                                                                                     61 ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
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/db_xref="taxon:9606"
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Porsch-Oezcueruemez, M.K.
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University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
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1 (bases 1 to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABC1 gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press 224 to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
                                                   1047 GCTTTGCTCCTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAA 1106
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                               61 ccgggctgcggcagggcagggcggggagctccgcgcaccaacagagccggttctcagggc 120
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On Jun 23, 2000 this sequence version replaced gi:7769713.
Location/Qualifiers
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/gene="ABCA1"
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Matches 221; Conservative
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Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
Resear,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
Regulatory nucleic acid sequences of the abcl gene
Patent: WO 0183746-A 1 08-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Schmitz,G. and Bodžioch,M.
Atp binding cassette transporter 1 (abc1) gene polymorphisms and
uses thereof for the diagnosis and treatment of lipid,
cardiovascular or inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2894 GTAATTGCGAGCGAGGGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTC 2953
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                        ggggtaggagaaagacgcaaacacaaaagtggaaaacag 221
181 ggggtaggagaaagagacgcaaacacaaaagtggaaaaacag 221
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100.0%; Pred. No. 5.3e-118;
Live 0; Mismatches 0;
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Sequence 1 from Patent W00183746.
AX351029
AX351029.1 GI:18616385
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/db_xref="taxon:9606"
773 c 876 g 773
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Sequence 3 from Patent WO0170810.
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AX253452.1 GI:16073979
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 5.3e-118;
iive 0; Mismatches 0;
                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
1765 c 1905 g 1756 t
Patent: WO 0170810-A 3 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
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                               Location/Qualifiers
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sections only once, except for a short overlap.
The true right end of clone RPI1-21787 is at 96717 in this sequence. The true left end of clone RPI1-1227F10 is at 72980 in this sequence. The true right end of clone RPI1-31320 is at 2000 in
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Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chinini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
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27673 a 21138 c 20380 g 27526 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derived from a single pUC clone. Restriction digest data confirm the assembly."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="Sequence from reads from a short insert library
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                                                                           {\tt IMPORTANT}: This sequence is not the entire insert of clone RPI1-217B7 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Sequence from AF275948 sequenced by National
Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
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Homo sapiens ABCAl (ABCAl) gene, complete cds.
AF275948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 221; DB 9; L
100.0%; Pred. No. 5.5e-118;
Live 0; Mismatches 0;
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Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
                                                                                                                                       2 (bases 1 to 149034)
Santamarina-Folo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois, T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (OB-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
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                                                                               Proc. Nat
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JOURNAL
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                                                                       JOURNAL
                                                                                                                                           REFERENCE
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                                                                                                             MEDLINE
                                                                                                                                                                                AUTHORS
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TITLE
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baltan, J., Barna, N., Beckerly, R., Boqualavkky, L., Boukhgalter, B., Bown, A., Castle, A., Collans, S., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McKernan, K., McGanghlin, J., Marquis, N., McKernan, K., McGanghlin, J., Marquis, N., Peterson, K., Pollarav, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 22, 2000 this sequence version replaced g1:6434033. All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M7815; 100% of reads Sequencing vector: M13; M7815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 117571 bases at least Q40 Consensus quality: 117571 bases at least Q30 Consensus quality: 160940 bases at least Q20 Insert size: 185000; agarose-fp Insert size: 171264; amm-of-contigs Quality coverage: 2.9 in Q20 bases; sum-of-contigs Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1004 1103: gap of 100 bp 1104 2634: contig of 1531 bp in length 2635 2734: gap of 100 bp 2735 4415: contig of 1681 bp in length 4416 4515: gap of 100 bp 4516 5785: contig of 1270 bp in length
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of 1707 bp in length
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of 1994 bp in length
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                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-1M10
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12354 15228: conti
15229 15328: gap of
15329 17200: conti
17201 17300: gap of
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7879: cor
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7980 9686; cor
                        (bases 1 to 175064)
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5886
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                                                AUTHORS
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JOURNAL
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Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1574 GCTTTGCTCCTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCCTTCTCCCGAAGGCTTGTCAA 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1454 GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCT 1513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 gctttgctccttgtttttccccggttctgttttctccccttctccggaaggcttgtcaa 180
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11arity 100.0%; Pred. No. 5.5e-118;
Conservative 0; Mismatches 0;
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AC012230.3 GI:7637254
HTG; HTGS_PHASE1; HTGS_DRAFT.
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54849. .54988
/rpt_family="Alu"
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61246. .61489
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44349. .44626
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                /rpt_family="Alu"
41657. .41679
/gene="ABCA1"
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13.132 13.131: gap of 100 bp 13.132 13.131: gap of 100 bp 13.138 13.139: contig of 6678 bp in length 13.136 145.49: contig of 73.32 bp in length 145.49 145.59: gap of 100 bp 145.52 15.739: contig of 13.10 bp 15.732 ls7.49: gap of 100 bp 15.732 ls7.49: gap of 175.73 bp in length 15.732 ls7.49: gap of 175.73 bp in length.
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                     22 20231: gap of 100 bp 22587: contig of 2356 bp in length 28 22687: contig of 2356 bp in length 28 25707: contig of 3020 bp in length 28 25807: gap of 100 bp 25807: gap of 100 bp 25834: gap of 100 bp 31338: contig of 3054 bp in length 35 28384: gap of 100 bp 31338: contig of 3054 bp in length
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68437: contig of 4676 bp in length

68537: gap of 100 bp

71558: gap of 100 bp

71558: contig of 2921 bp in length

76888: contig of 5330 bp in length
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103016: contig of 5015 bp in length
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42835: contig of 4417 bp in length
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contig of 4402 bp in length
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20131: contig of 2831 bp in length
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88220: cont
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52618: cont
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56592: cont
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Arian 2014 bp DNA linear PRI 29-APR-2001 Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1) and SNAP protein genes, complete cds.
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SOURCE

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Junior 1. 18476,72893. .72986,77520. .77661,78931. .79049, 101048. .101169,104152. .104328,117287. .117379, 101048. .101169,104152. .104328,117287. .117379, 122329. .122569,125285. .125424,125754. .125870, 130079. .139390,135677. .135898,136599. .131925, 131709. .139390,135677. .135898,136599. .131025, 131709. .139310,135677. .135898,136599. .141471, 145219,143123. .142360,143963. .144183, 145241. .145813,146677. .146389,148277. .14884,150280. .156747, 152202, 153438. .155374,160847. .160942,166417. .162491, 160912, 166417. .162491, 166818. .166829,168905, 168628. .166703, 170109. .170229,17017. .171079,171987. .172093, 174448. .174589,174761. .175095,176019. .176625. .176717, 177376. .177619,178500. .178700)
                                                                                                                                                                                                                                                     2 (bases 1 to 201144)
Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                           1 (bases I to 2014)
Olu,Y., Caveller,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse aboal comparative sequencing and transgenesis studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                      Homo sapiens
                                            human.
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REFERENCE
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TITLE
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exon

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exon

'number=14

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SRANICAAACGGIIYFTLILEPYULCVARODYVOGTIKIFASILISPYAGEGECECFALEE
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NAILRANLQKGSNYSTLILLLATGWSTTAMYRATODTSVVLTSVNLFIGINGSVY
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REGERENTERGENTERGENTERGENTERGENTERGY
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PEREWGRYGFFALLTGNYN GENYBROTTGNYN GRONTRANT NKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVYEQAIIRVLTGTEKKTGVYMQQMPY PCYVDDIFLRVWSRSMPLFWTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLF GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE **JOLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN** KLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT MDPKARRFLMNCALSYVKEGRSYVLTFHSMEECFALCTRMAIWINGRFRCLGSYQHLK NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARI FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDOSDDDHLKDLSLHKNQTVVDVAVLT SFLQDEKVKESYV" 72893. .72986

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New Doublished (2000)

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AK024328
AK024328.1 GI:10436685
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               PRI 29-SEP-2000
                                                                                                                                                                                                                                                                              Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A. NEDO human cDNA sequencing project
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMA1
clone:MAMMA1000851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.1%; Score 219; DB 9; Length 1750; Best Local Similarity 100.0%; Pred. No. 7.8e-117; Matches 219; Conservative 0; Mismatches 0; Indels
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AK022254
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1. .1750
                                                                                          AK022254.1 GI:10433612
                                                                                                                                                                                             Homo sapiens
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AUTHORS
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100.0%; Pred. No. 5.5e-118;
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/gene="ABCA1"
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/gene="ABCA1"
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/gene="ABCA1"
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ACCESSION VERSION

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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomicsEthi.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert construction, 5-6 3-end one pass sequencing and clone selection: Helix Research Association for Biotechnology; cDNA library Helix Research Institute (supported by Japan Key Technology Center University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MACWPOOLRLLAWKNLTFRRRQTCOLLLEVAWPLFIFLILISVRL
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NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
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LLSICASVPKVEFHERHILEHFSFCVCVSVSLFPAKGIVSFSWASFRIWVLWRAVFWQ
HGESMAVWEGQLGLGLNIAFEYFTSIDVG"
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2 (bases 1 to 1556)
Isogai, T. and Otsuki, T.
Direct Submission
                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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oligo capping; fis (full insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1002437.
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314. .1405
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                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 9854)
Denefie, P., Rosier-Montus; M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remalcy, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Butherla;

I (base; Ito 9854)

Benefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,

Naudin, L., Lemoine, C., Duverger, M., Jaye, M., searfoss Iii, G.H.,

Nucleics acids of the human abcl gene and their therapeutic and angenositic application

Patent: EP 1096012-A 70 02-MAY-2001;

Aventis Pharma S.A. (FR)

Location/Qualifiers
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/db_xref="taxon:9606"
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Signature, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, S., Badawin, J., Barna, N., Beckerly, R., Beda, F., Bodeslavkiy, L., Boukhaller, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Lolangelo, M., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzlugh, W., Forrest, C., Gale, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Merban, P., McGurk, A., McKernan, K., McRentan, C., Connor, T., O'Connor, P., Mordurk, A., McKernan, K., Norman, C.H., O'Connor, T., O'Connorll, P., Olivar, T. M., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Savery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vasslilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dirnert, S., Linder, A., Wasslilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dirnert, S., Linder,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 13-JUL-2000
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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   92.8%; Score 205; DB 6; Lv 100.0%; Pred. No. 1.2e-108; ive 0; Mismatches 0;
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contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                          However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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23780: contig of 848 bp in length
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65740: contig of 857 bp in length
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Manda, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceride levels

Patent: WO 0115676-A 108-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)

Location/Qualifiers
                                                                                                                                                                                                                                                                     Db 41565 GTAATTGCGAGCGAGGTGAGTGGGGCCGGGACCCGCAGGCCGAGCCGACCCTTCTCTC 41624
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                                                                                          Score 201; DB 2; Length 69570;
Pred. No. 2.8e-106;
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65741 65840: gap of 100 bp
65841 66684: contig of 844 bp in length
66685 66784: gap of 100 bp
66785 67651: contig of 867 bp in length
67652 67751: gap of 100 bp
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/db_xref="taxon:9606"
49549 a 37944 c 41170 g 54950 t
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Matches 201; Conservative
                                                                                        Query Match
Best Local Similarity 100.
Matches 201; Conservative
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Lawn, R. M., Wade, D., Oram, J. F. and Garvin, M.
Atp binding cassette transporter protein abol polypeptides Patent; Wo 0078971-A 1 28-DEC-2000;
CV THERAPEDICS, INC. (US)
                                                                                                                 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10442)
1 (bases 1 to 10442)
1 Adam, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abcl
Patent: WO 0078972-A 1 28-DEC-2000;
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100.0%; Pred. No. 5.9e-104;
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/db_xref="taxon:9606"
2297 c 2408 g 2835
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/db_xref="taxon:9606"
1 2297 c 2408 g 2835
                    Sequence 1 from Patent WO0078972. AX060713
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/translation="MGWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLLISVRL
SYPPYEQHECHFPNKAMPSAGTLPWVQGIIONANNPCFRYPTPGEAPGVVGRFNKSIV
ARLESDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLODFLVDNETPSGFLYH
NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEBMIQLGDQDEVSELYELY
KEKLAAAERVLRSNNTLKPILRTLNSTSPPESKELAEATKTLHSLGTAQELFSMR
SWSDMRQEVMFLINVNSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
RQVMAEVNKTFQELAVFHDLEGWMETSPPENSTIWKALKRLLVGKILYPPDTPAT
RQVMAEVNKTFQELAVFHDLEGWMETSPPENSTRIWKALRLLDSRDNDHFWE
OOLDGLDWTAQDIYARTAKHPEDVQSSNGSYTWFREAFRETTRRFISKBNDHFWE
COLDGLDWTAQDIYARTAKHPEDVQSSNGSYTWFREAFRETTRRFISKBNDDHFWE
REFIATEVMLINKSMELLDERKFWAGIVFTGITPGSIELPHYVKYKIRMDIDNVERF
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SRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFASLLSPVAFGFGCEYFALFE
EQGIGVQWDNLFESPVEEDGFNLTTSISWMLFDTFLYGVWTWYIEAVFPGQYGIPRPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, complete cds.
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PCYVDDIFLRVWSRSMPLFWTLAWIYSVAVIIKGIVYEKEARLKETMRILMGLDNSILW
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AVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIR
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Zudan, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.

Direct Submission
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA

Location/Qualifiers
                                                                                        gttctgttttctccccttctccggaaggcttgtcaaggggtaggagaaagagacgcaaac 204
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25 ggccgggacccgcagagccgagccgaccttctctccccgggctgcggcagggcagggcgg
                                       1 GGCCGGGACCCGCAGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGCGG
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/db_xref="G1:9755159"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Garelara, P., FitzHugh, W., Forrest, C., Gaqe, D., Galagan, J., Gartyna, S., Grant, G., Hagos, B., Hadsord, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliais Euthenia; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 90698) ACO21345 90698 bp DNA linear HTG 1 Homo saplens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING. ACO21345 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-24J9 Unpublished AC021345.2 GI:9130845 (bases 1 to 90698) HTG; HTGS\_PHASEO Homo sapiens human. AC021345/c DEFINITION ORGANISM ACCESSION JOURNAL REFERENCE KEYWORDS SOURCE AUTHORS REFERENCE AUTHORS VERSION LOCUS

HTG 13-JUL-2000

Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Myman, D., Ye, W.J., Direct Submission Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced 91:6705761. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research \* NOTE: This record contains 92 individual
sequencing reads that have not been assembled into
scontigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
\* However, it should not be assumed that this clone
\* will be sequenced to completion. In the event that Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence\_submissions@genome.wi.mit.edu the record is updated, the accession number will 2824; contig of 851 bp in length 2825 2924; agap of 100 bp 3802; contig of 878 bp in length 3803 3902; gap of 100 bp 4816; contig of 679. 7. gap of 100 bp 7. gap of 883 bp in length 7: gap of 100 bp 100 bp of 908 bp in length 9853: gap of 100 bp 10757: contig of 904 bp in length 10857: gap of 100 bp 11732: contig of 875 bp in length 11832: gap of 100 bp 12739: contig of 907 bp in length of 100 bp contig of 843 bp in length of 100 bp contig of 905 bp in length 910: contig of 910 bp in length 911 1010: gap of 100 bp 1011 1873: contig of 863 bp in length contig of 898 bp in length in length in length 839: gap of 100 bp 13710: contig of 871 bp in 810: gap of 100 bp 14684: contig of 874 bp in 784: gap of 100 bp 15662: contig of 878 bp in 100 bp 915 bp 77: gap of 100 bp 17678: contig of 901 bp 17679 17778: gap of 100 bp 17779 18679: contig of 901 bp 18680 18779: gap of 100 bp 100 bp Project Information Center project name: L4483 Center clone name: 24\_J\_9 : contig of 12740 12839; gap of 12840 13710: contig cont 24: gap of 16677. 6: gap of 5759: con gap of 8855: gap of , 6864: gar 7747: c 9753: 9854 1075 10758 10857: 10858 1173: 11733 11832: 11833 1273: 7748 7847: 9 7848 875 13711 13810: 14784: 15762: 16777: 5859; be preserved. 4917 5760 6765 13811 14685 14785 15663 15763 TITLE JOURNAL COMMENT

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 10474)
Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abcl
Patent: Wo 007091972-A 7 28-DEC-2000;
CV THERAPEDTICS, INC. (US)
Location/Qualifiers
1 . .10474
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55306: gap of 100 bp
56165: contig of 859 bp in length
56265: gap of 100 bp
57124: contig of 859 bp in length
5724: gap of 100 bp
58121: contig of 897 bp in length
                                                                                                                                                                                                                                                                58221; gap of 100 bp 59075; contig of 854 bp in length 59175; gap of 100 bp 60058; contig of 883 bp in length 60158; gap of 100 bp 61067; contig of 909 bp in length 61067; contig of 909 bp in length
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.

Atp binding cassette transporter protein abc1 polypeptides
Patent: Wo 0078971-A 9 28-DEC-2000;

CV THERAPEUTICS, INC. (US)

Location/Qualifiers
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1 (bases 1 to 446)
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iii,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human abcl gene and their therapeutic and
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1 (bases 1 to 446)
Denefile, Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Nucleic acids of the human abcl gene and their therapeutic and
parent: WO 0130848-A. 3 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Patent: EP 1096012-A 3 02-MAY-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 9741)
Denefle, P., Rosier-Montus, M. F., Arnould-Requigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Nucleic acids of the human abcl gene and their therapeutic and agagnostic application
Patent: WO 0130848-A 69 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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/note="Oligonucleotide Primer"
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Sequence 69 from Patent W00130848.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searfoss Iii, G.H., Remaley, A., Brewer, H.B. and Dean, M.
Nucleics acids of the human abcl gene and their therapeutic and diagnostic application
Patent: EP 1096012-A 69 02-MAY-2001;
Aventis Pharma S.A. (F.R.)
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Sequence 10 from Patent W00183746.
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
2180 c 2290 g 2620
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AX060715.1 GI:12406104
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1643)
Lawn, R.M., Wade, D. and Garvin, M.
Lawn, R.M., Wade, D. binding cassette transporter protein abcl Patent: WO 0078972-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
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Atp binding cassette transporter protein abc1 polypeptides
Patent: WO 0078971-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
AC021246.2 GI:9119882
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Pred. No. 6.4e-42;
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/db_xref="taxon:9606"
413 c 457 g 400
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173 18041: contig of 869 bp in length 142 18141: gap of 100 bp in length 142 19009: contig of 868 bp in length 110 19109: gap of 100 bp in length 10 19966: contig of 867 bp in length 67 20066: gap of 100 bp
9431 9530: gap of 100 bp 9531 10376: contig of 846 bp in length 10477 10476: gap of 100 bp 10477 11322: contig of 846 bp in length 11323 11422: gap of 100 bp 11323 12402: gap of 100 bp 12403 12402: gap of 100 bp 12403 13380: contig of 878 bp in length 13381 13380: contig of 878 bp in length 13381 1341: gap of 100 bp 1441: contig of 861 bp in length 15197 15296: gap of 100 bp 15197 15296: gap of 100 bp 15197 15296: gap of 100 bp 15197 15296: gap of 100 bp 15197 15296: gap of 100 bp 15197 15296: gap of 100 bp 15197 15296: gap of 100 bp 15297 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 15197 
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42824: contig of 811 bp in length
42924: gap of 100 bp
43776: contig of 852 bp in length
43876: gap of 100 bp
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33312: contig of 844 bp in length
3412: gap of 100 bp
34268: contig of 856 bp in length
34368: gap of 100 bp
35204: contig of 836 bp in length
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17073 17172: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted Mass. 2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 69570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2512
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of 100 bp
contig of 844 bp in length
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                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-1N10
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Web site: http://www-seq.wi.mit.edu
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                                                  human.
Homo sapiens
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              KEYWORDS
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COMMENT

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Submitted (18-007-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 92227) Waterston,R.H.
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Homo sapiens chromosome, clone RP11-3123
Unpublished
2 (bases 1 to 149710)
2 (bases 1 to 149710)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Ferrelra, P., FitzHugh, W., Forrest, C., Gage, D.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 149710)
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HOMO saplens clone RP11-3L23, LOW-PASS SEQUENCE SAMPLING
AC022563
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Contact: submissions@watson.wustl.edu
Project Information
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/clone="RP11-485017"
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   The sequence of Homo sapiens clone Unpublished
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 92227)
Waterston, R. H.
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                       3. 44852: 392 of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp
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44752: contig of 876 bp in length
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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGlerk, A., McKennan, K., McPheeters, R., Marquis, N., McEwan, P., McGlerk, J., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Lessearch, J. Conter for Genome Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6910806.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1995-1997)
                                                                                                                                                                                                                                                                                                            ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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11663: contig of 684 bp in length
11763: gap of 100 bp
12433: contig of 670 bp in length
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41759: gap of 100 bp
42434: contig of 675 bp in length
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2 Edases 1 to 162496)

8 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bodustavkiy, L., Boduknalter, B., Brown, A., Burkett, G., Castle, A., Castle, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, R., Diaz, J. S., Dodge, S., Domino, M., Porteira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gradyna, S., Ginde, S., Goyette, M., Graham, L., Gradyna, J., Lakocque, K., Lamazares, B., Haeflord, A., Horton, L., Howland, J.C., Iliew, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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07: gap of 100 bp
43980: contig of 673 bp in length
80: gap of 100 bp
4768: contig of 688 bp in length
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700 bp in length
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contig of 688 bp in length
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55702: contig of 681 bp in length
102: gap of 100 bp
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51915: contig of 688 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 10, clone RP11-524H12 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                          47943: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT.
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55703 55802: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 55886 AGCTTGTCAAGGGGTAGGA 55905
                                                                                                 44868: gap of
                                                                                                                                                  45656: gap of
                                                                                                                                                                                                                                                   gap of
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Matches 20; Conserv
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Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Santos,R., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J., Vassillev,H., Viel,R., Vol., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J., Zimmer,A. and Zody,M.
Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.960731
Consensus quality: 154128 bases at least Q40
Consensus quality: 158489 bases at least Q30
Consensus quality: 160079 bases at least Q30
Insert size: 163000; agarose-fp
Insert size: 16096; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                 All repeats were identified using RepeatWasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M77815; 100% of reads Chemistry; Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20: gap of 100 bp
70481: contig of 12461 bp in length
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contig of 23076 bp in length
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contig of 11153 bp in length
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contig of 22103 bp in length
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982 4366: contig of 3385 bp in length

4367 4466: gap of 100 bp

4467 7420: contig of 2954 bp in length

7421 7520: gap of 100 bp

7521 11683: contig of 4163 bp in length
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47838: cont
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113943: con
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91741
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36586
36686
47839
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JOURNAL
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100 bp

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228703 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus chromosome SA clone CH230-152G15, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
                                                                           Submitted (133-007-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 31, 2000 This sequence version replaced gi:7690207.
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than a error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                 Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                    Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 3343: contig of 3343 bp in length
* 3344 40628: contig of 7185 bp in length
* 40629 40728: gap of unknown length
* 40729 143349: contig of 102621 bp in length
* 14350 14349; contig of 102621 bp in length
* 14350 144499: contig of 1050 bp in length
* 144500 144599: gap of unknown length
* 144500 14659; agap of unknown length
* 14600 162264: gap of unknown length
* 162265 162364: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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gap of unknown length
contig of 13982 bp in length.
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54511 a 50297 c 47816 g 48714 t
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/db_xref="taxon:9606"
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                   2 (bases 1 to 201938)
DOE Joint Genome Institute.
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Matches 20; Conservative
                                                                Direct Submission
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187957
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AC097253/c
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                     REFERENCE
AUTHORS
TITLE
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                                                                                 JOURNAL
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Catarrhini; Hominidae; Homo.
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162496: contig of 25277 bp in length.
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
1 33487 c 33493 g 46593 t
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/note="assembly_fragment"
70582. .80819
/note="assembly_fragment"
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47939. .57920
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/note="assembly_fragment"
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/note="assembly_fragment"
114044. .137119
/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment
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                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 201938)
DOE Joint Genome Institute.
                     Location/Qualifiers
1. .162496
                                                                                                                                           /clone="RP11-524H12"
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15365. .20920
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982. .4366
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TITLE
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AC012325
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 05-MAR-1997
Quality coverage: 6.4x in Q20 bases; sum-of-contigs estimation
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Dembic, Z., Garotta, G. and Gentz, R.H.
Chimeric human interferon-gamma-receptor/immunoglobulin
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Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                  contig of 40920 bp in length
contig of 32809 bp in length
gap of unknown length
gap of unknown length
contig of 26213 bp in length
gap of unknown length
gap of unknown length
contig of 26739 bp in length
gap of unknown length
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Other publication JP 6319552 941122
Other publication NZ 250997 951026
Other publication CA 2114168 940906
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Patent: EP 0614981-A 2 14-SEP-1994;
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Sequence 2 from Patent EP0614981.
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Muzny, D.M., Adans, C., Adio-Oduola, B., All-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., Harla, M., Harlak, B., Hanilton, K., Harris, G., Harris, G., Harris, K., Harris, G., Harris, K., Harris, C., Harris, K., Harris, C., Harris, R., Harris, G., Harris, K., Harris, C., Harris, R., Harris, G., Karlvori, J., Kures, D., Houlow, S., Huber, J., Hulyk, S., Hume, J., Jankson, E., Kally, S., Khan, U., Karson, E., Kally, S., Khan, U., Karson, E., Mawhiney, B., Mchen, G., Martinda, E., Li, J., Li, Z., Li, Z., Lu, X., Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17062530.
                                                                                                                                      Eukaryota, Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 221817 bases at least Q40 Consensus quality: 223045 bases at least Q30 Consensus quality: 223446 bases, at least Q20 Estimated insert size: 224711; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation
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Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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2 (bases 1 to 228703)
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Rattus norvegicus
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KARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVD
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GVLHYWGVTTEKSKRVCITIENSSIRGSLMIPVVAALLLFIVLSLVRICFYIKKINPL
KERSIILDKSLISVVRSATLETKPESKYVSLITYQPSLEKEVVCEBPLSPATVPGM
HTEDDPGKVEHTEELSSITEVVTTEENIPDVVPGSHLTPIERESSSPLSSNQSEPGSI
ALNSYHSRNCSESDRNGFPDSSCLESHSSLSDSRFPPNNKGEIKTEGQELITVIK
APTSFGYDKPHVLVDLLVDDSGKESLIGYRPTEDSKEFS"
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Homo sapiens clone YAN1 interferon-gamma receptor mRNA, complete
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1 (bases 1 to 1641)
Allende,L.M., Lopez-Goyanes,A., Paz-Artal,E., Corell,A., Carcia-Perez,M.A., Varela,P., Scarpellini,A., Negreira,S., Palenque,E. and Arnaiz-Villena,A.

A point mutation in a domain of gamma interferon receptor 1 provokes severe immunodeficiency
Clin. Diagn. Lab. Immunol. 8 (1), 133-137 (2001)
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Arnalz-Villena,A.
Direct Submission
Submitted (02-APR-1998) Immunology, Hospital 12 de Octubre, Crta.
Andalucia Km. 5,4, Madrid 28041, Spain
Location/Qualifiers
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/cell_type="lymphocyte"
/tissue_type="blood"
22. .1491
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           Other publication CN 1094092 941026
Other publication AD 5647849 940908
Other publication ZA 9401333 940906.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="YAN1"
                                                                                1. .735
/organism="unidentified"
                                                                                                                   /db_xref="taxon:32644"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2064)
Aguet,M., Dembic,Z. and Merlin,G.
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( chases 1 to 1773)

Hirsch, V. M., McGann, C., Dapolito, G., Goldstein, S., Ogen-Odoi, A., Biryawaho, B., Lakwo, T. and Johnson, P.R.
Identification of a new subgroup of SIVagm in tantalus monkeys Virology 197, 426-430 (1993)
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100.0%; Pred. No. 8.8;
tive 0; Mismatches 0; Indels (
            Length 1641;
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Homo sapiens
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100.0%; Pred. No. 8.8;
tive 0; Mismatches 0
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Simian immunodeficiency virus DNA.
Simian immunodeficiency virus
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YDPFTTCT:TRYNNYWYRWNGSEIQYKILTQREDDCDEIQCQLAIPVSSLNSQYCVSAE
GVLHVWGVTTEKSKEVCITIFNSSIKGSLWIPVVAALLLFLVLSLVFICFYIKKINPL
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TEDNGKVREHTEELSSITEVTTEBAT PDVVPGSHLTPIERESSPLSSNOSBPGSI
ALNSTHSRNCSESDBSRNGFDTDSSCLESHSSLSDSFPPNNKGEIKTEGGELITVIK
APTSEGYDKPHVLVDLLVDDSGGESLIGYRPTEDSKEFS"
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      passed the following selection criteria: matched mRNA gi: 5419821.
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Pred. No. 8.8;
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100.0%; Pred. No. 8.8;
tive 0; Mismatches 0; Indels
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                                                                                                            /db_xref="taxon:9606"
/clone="MGC:12420 IMAGE:3950528"
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H.saptens pBABLUE SacI/Asp7181 fragment.
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413 c 452 g 631
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                                                                                                                                                        /tissue_type="Prostate"
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                             Location/Qualifiers
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-spac.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                    KARVGQKESAYAKSEEFAVCRIGKIGPPKLDIRKEEKQIMIDIFHPSYFVNGDEQEVD
YDPETTCYIRVYNVYVRMNGSELQYKILTQKEDDCDEIQCQLAIPVSSLNSQYCVSAE
GVLHVWGVTTEKSKEVCITIFNSSIKGSLMIPVVAALLLFLVLSLVFICFYIKKINPL
                                                                                                                                                                                                                                                                                                                                                                                                                                      KEKSIILPKSLISVVRSATLETKPESKYVSLITSYQPFSLEKEVVCEBPLSPATVPGM
HTEDNPGKVEHTEELSSITEVVTTEENIPDVVPGSHLTPIERESSSPLSSNQSEPGSI
ALNSYHSRNCSESDHSRNGFDTDSSCLESHSSLSDSEFPPNNKGEIKTEGQELITVIK
                                                                                                                                                                                                                                                                                                       /db_xref="GDB:G00-120-688"
/translation="MALLFLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNP
IVYWEYQIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2127 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, interferon gamma receptor 1, clone MGC:12420
BC005333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2127)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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1 bp upstream of EcoRI site; chromosome 6q15-q21.
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                                                                                                                                                                                                                   /note="interferon-gamma receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                          /product="IFNR-gamma mRNA"
                                                                                                                                                                                                                                                           /protein_id="AAA52731.1"
/db_xref="G1:306915"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pr
                                             /map="6q23-q24"
                                                                                                                                          /gene="IFNGR1"
49. .1518
                                                                                      /gene="IFNGR1"
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